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9, 2003, 17:07:01 ; Search time 39.4564 Seconds (without alignments) 1198.803 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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SUMMARLES	DB ID Description	3 19 AAW85457	22 AAU00512	3 23 ABP61801 Human polymentide	19 AAW75220	23 AAE26983	23 AAE27121	24 ABR47926	24 ABU64994	24 00000 80
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ALIGNMENTS

AAW85457 standard; Protein; 298 AA. (first entry) 25-FEB-1999 AAW85457;

AAW85457

Secreted protein encoded by clone ct864_4.

Secreted protein; nutritional activity; immune stimulating; vaccine; suppressing activity, haematopoiesis regulating activity; ctisque growth activity; activin; inhibin activity; chemoteataxis; chemokineis activity; haemostasis; thrombolytic activity; receptor; ligand; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy

98WO-US05653. 98US-0044466. 97US-0822167. Homo sapiens 19-MAR-1998; 21-MAR-1997; WO9842739-A2 20-MAR-1998; 01-OCT-1998.

Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D; Racie LA, Spaulding V, Treacy M; (GEMY) GENETICS INST INC.

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                                                                                                                                                                                                           The present sequence represents a secreted protein. The polymucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating activity, tissue svaccines) or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, activin/inhibin activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, anti-inflammatory activity and because special properties of the specification to support these activities). The polynucleotide is also stated to be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
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                                                                                    New polynucleotides encoding secreted human proteins - derived from human foetal brain, adult brain, foetal kidney, placenta or adult pineal gland cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Junctional adhesion protein; JAM2; cellular localisation; cellular expression; immunoprecipitation; stroke; phosphorylation; glycosylation; paracellular migration; inflammatory disease; arthritis; asthma; rheumatoid arthritis; inflammatory bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 1518; DB 19; Length 298; 99.3%; Pred. No. 1.1e-118; ive 0; Mismatches 2; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human junctional adhesion protein (JAM2).
                                                                                                                                                                          Claim 17; Page 73-74; 113pp; English.
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les 296; Conservative
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                       WPI; 1998-609890/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents a human junctional adhesion molecule 2 (JAM2). The polymucleotide encoding the polypeptide is useful for recombinant production of JAM-2 protein, which in turn is useful for the production of antibodies. The antibodies may be used for probing cellular localisation and/or expression of JAM2 in tissues under normal and disease states, for immunoprecipitating JAM2 protein from cells and/or stroke tissues to determine whether it is modified by glycosylation and phosphorylation, and for determining JAM2 function. The antibodies inhibit interaction of JAM2 with inflammatory cells or influences their paracellular migration, and is therefore useful for alleviating inflammatory diseases such as arthritis, asthma, rheumatoid arthritis, inflammatory bowel disease and Crohn's disease.
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                        29.298

70ncte= "Possible mature JAM2 #2"

237.254

/note= "Transmembrane domain"
/note= "Possible mature JAM2 #1"
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such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention.

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Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antiinflammatory; antibacterial; immunosuippressive; antiparkinsonian; neurinflammatory; antibacterial; immunosuippressive; antiparkinsonian; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; cytokine; call proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; alzheimer; disease; parkinson's disease; huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.
Human polypeptide SEQ ID NO 155
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Homo sapiens

US2002065394-A1

30-MAY-2002

22-DEC-2000; 2000US-0745763

98US-0040963 18-MAR-1998;

JACOBS K. JACO/)

MCCOY J M. LAVALLIE E F

LAVALLIE E R. COLLINS-RACIE LAVA/ COLL/

EVAN/

EVANS C. MERBERG D. TREACY M. (TREA/) (SPAU/) MERB/)

SPAULDING V.

Evans C; Collins-Racie LA, LaVallie ER, Spaulding V; Treacy M, McCoy JM, . a Jacobs K, Merberg

2002-582343/62 N-PSDB; ABQ92017 Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis

Claim 54; Page 116-117; 284pp; English.

The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic caid (CDNA) inserts (II), where the protein is substantially free from cother mammalian proteins. (I) are useful for preventing, treating or meliorating a medical condition, cepecially immunological treatment or conference (II) are useful for preventing, treatment or conference (II) are useful factor artinflammatory, stem cell proliferation, cell differentiation, antinflammatory, cytokine, cell proliferation, cell differentiation, antinflammatory, conference (II) can be used to manipulate stem cells in culture to give contropithelial cells that can be used to augment or replace cals damaged by illness, autoimmune disease, accidental damage or rise to neuroepithelial cells that can be used to augment or replace contropithelial cells that can be used to augment of nerve and brain tissue and is useful for the treatment of genetic disorders. (I) induces the proliferation of neural cells and central and peripheral nervous system diseases and neuropathies, such as a certain and peripheral nervous system diseases and neuropathies; contact and peripheral nervous system diseases and neuropathies; cativity, regulation of haematopoiesis and is useful for treating myeloid cell disorders, platelet disorders such as thrombocytopaenia contingue growth and in tissue repair, healing of burns, incisions, incision or tesure combined disorders, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,

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                                                                                                                                                                                                                                   LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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                                                                                                                                                                                                                                                                                          LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                                                                                       121 LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                                                                                                                                       diagnosis, tissue, cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer; disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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                                                                                                                                                                                                                                                                                                                                                                                                                              241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                           1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; fusion protein; gene therapy; protein therapy
                                                                                                                                                                                        1 MARRSRHKLILLILRYLVVALGYHKAYGFSAPKDQQVVTAVEYQBAILACKTPKKTVSSR
                                                                                                                                                                                                                                                                                                                                                    LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
                                                                                                                                                  Gaps
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                                                                                                                  99.8%; Score 1518; DB 23; Length 298; 99.3%; Pred. No. 1.1e-118; ive 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein encoded by gene 25 clone HTEEB42.
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97US-0040762.
97US-0048100.
97US-0048189.
97US-0048357.
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                                                                                                                                Best Local Similarity 99.3
Matches 296; Conservative
                                                                                     298 AA;
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14-MAR-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
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Ruben SM,
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(FISC/)
(LIHH/)
(SOPP/)
(GENT/)
                                                                                                                                                    Peptide
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(LIYY/)
(ZENG/)
                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                          RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WEIY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soppet
  This sequence represents a secreted human protein encoded by the gene fullone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic acid sequences: AAV34245; amino acid sequences AAV354596-V34325; amino acid sequences AAV35496-V34335) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 28 polynucleotides, based on which tissues they are most highly expressed in (see AAV34286 for described uses).
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autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
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                                                                                                                                      Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 298;
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                                                        Greene JM, Kyaw H;
Ruben SM, Soppet DR;
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100.0%; Pred. No. 1.4e-118;
iive 0; Mismatches 0;
                                                                                                                                                                                    Claim 1; Page 168-169; 201pp; English.
                                                       Fischer CL, Gentz RL,
, Moore PA, Rosen CA,
ung PE, Zeng Z;
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                                   (HUMA-) HUMAN GENOME SCI INC
  97US-0048970.
97US-0057765.
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Best Local Similarity 100.
Matches 298; Conservative
                                                                                                     WPI; 1998-520811/44.
                                                                              Young PE,
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                                                                                                                N-PSDB; AAV34310.
                                                      Ferrie AM, F
Li H, Li Y,
  06-JUN-1997;
             05-SEP-1997;
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Wei YF,
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Abb44636-AAb44676 represent cDNAs corresponding to 28 human secreted protein genes, and AAE26959-AAE2699 represent the proteins they encode. AAE37009-AAE37025 represent human secreted protein fragments or their variants. The secreted proteins and genes estul fragments or their variants. The secreted proteins and genes engeful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed and include developing products for the disgnosis or treatment of immunodeficiencies, e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies autoimmune disorders e.g., systemic lupus erythematosus, rheumatoid arthritis, multiple solerosis, autoimmune trythematosus, rheumatoid arthritis, multiple solerosis, autoimmune crythematosus, rheumatoid arthritis, multiple solerosis, autoimmune crythematosis, autoimmune haemolytic anaemia, Goodpasture's syndrome, crave disease, diabetes mellitus, dermatitis, inflammatory conditions including septic shock, sepsis, reperfusion injury, inflammatory bowel disease, crohn's disease, haematopoletic disorders, respiratory disorders e.g., asthma and allergy, gastrointestinal disorders e.g.,
respiratory disorder; asthma; allergy; gastrointestinal disorder; inflammatory bowel disease; neurodegenerative disorder; hepatitis; parkinson's disease; Alzheimer's disease; carddovascular disorder; atherosclerosis; myocarditis; renal disorder; fungicide; virucide; hyperproliferative disorder; acute glomerulonephritis; tonsilitis; respiratory disorder; rinitis; sinusitis; neurological disease; endocrine disorder; Addison's disease; reproductive system disorder; endometriosis; vasotropic; vulnerary; cytostatic; nootropic; cardiant; anti-HIV; tranquilliser; gout; antiparasitic.
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, Moore PA, Young PE, Greene JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/note= "Encoded by
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Wei Y,
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Gentz RL,
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ZENG Z.
KYAW H.
FISCHER C L.
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ROSEN C A.
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/note= "Encoded by TSC"

/label= Unknown

Misc-difference 58

US2002076756-A1

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inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and breast), central nervous system (CNS) disorders e.g., ischaemic brain injury and/or stroke, neurodegenerative disorders e.g., Parkinson's disease and Alzheimer's disease, AIDS-related dementia and prion disease, cardiovascular disorders e.g., myocarditis, arrhythmias, atheroscilerosis, inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis, sarcoidosis and allogenic transplant rejection, bloodrelated disorder (thrombosis, arterial thrombosis, atheroscilerosis), hyperproliferative disorders, respiratory disorders e.g. rhinitis, hyperproliferative disorders, respiratory disorders, pneumonitis, renal disorders. e.g. acute glomerulonephritis, neurological diseases, liver disorders, endocrine disorders e.g., hyperthyroidism, Addison's disorders e.g. endometriosis. The present sequence represents a human disorders e.g. endometriosis. The present sequence represents a human construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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Pred. No. 1.4e-118;
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100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                         Sequence
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Human, secreted protein, autoimmune disease, hyperproliferative disorder, rheumatoid arthritis, neoplasm, cerebrovascular disorder, angiogenesis, cerebral ischaemia, cardiovascular disorder, nervous system disorder, cardiac arrest, Alzheimer's disease, ocular disorder, wound healing, infection, corneal infection; skin aging, food additive, preservative, tissue regeneration; immunosuppressive, antiproliferative, cychostatic, cardiant, vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial; virucide; fungicide; ophthalmological; gene therapy;
                                                                                                                    Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
                    AAE27121 standard; Protein; 298 AA
                                                                                   (first entry)
                                                                                   13-DEC-2002
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                   AAE27121;
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120

61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGON

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/label= Signal_peptide 23..298 /note= "Mature human secreted protein"

Location/Qualifiers

Peptide Protein /note= "Encoded by GWG"

/label= Unknown

Misc-difference

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protein genes, and AAE27014 represent the proteins becreed
AAE27138-AAE27164 represent human secreted protein fragments. The genes
and their corresponding secreted proteins are useful for preventing,
treating or ameliorating medical conditions, e.g., by protein or gene
therapy. Secreted protein sequences of the invention are useful for the
diagnosis or treatment of disorders such as autoimmune diseases (e.g.
theumatoid arthritis), hyperpoliferative disorders (e.g. neoplasms of
the breast or liver), crebrovascular disorders (e.g. cardiac arrest), nervous
system disorders (e.g. dafaheimer's disease), infections caused by fungi,
angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
system disorders (e.g. Alzheimer's disease), infections caused by fungi,
bacteria and viruses and ocular disorders (e.g. corneal infection). The
polypeptides can also be used to aid wound healing and epithelial cell
proliferation, to prevent skin aging due to sunburn, to maintain organs
to regenerate tissues and in chemocaxis. They can also be used as food
additives or preservative to increase or decrease storage capabilities,
additives or preservative to increase or decrease storage capabilities,
and other mutrificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         components. The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for diagnosing, preventing, treating or ameliorating medical conditions and as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      äË,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                     Li Y, Zeng Z, Kyaw H, Fischer CL,
Wei Y, Moore PA, Young PE, Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.7%; Score 1517; DB 23; 100.0%; Pred. No. 1.4e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 186-187; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.,,
100.0%; Pre
                                                                                                                                                 02-FEB-2001; 2001US-265583P
                                                                                                                     11-MAY-2001; 2001US-0853161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity .... Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-574454/61.
N-PSDB; AAD44878.
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                                                                                                                                                                                                                                                                                SOPPET D R.
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YOUNG P E.
                                                                                                                                                                                                                                                                                                                                                         GREENE J M.
FERRIE A M.
                                                                                                                                                                                                                                                                                                GENTZ R L.
WEI Y.
                                                                                                                                                                             RUBEN S M.
ROSEN C A.
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                                                                                                                                                                                                                       ZENG Z.
KYAW H.
                                                                                         20-JUN-2002
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Ferrie AM;
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Soppet DR,
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(GREE/)
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(FISC/)
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LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN

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Gaps

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Length 298; Indels

99.7%; Score 1517; DB 24; 100.0%; Pred. No. 1.4e-118; ive 0; Mismatches 0;

298 AA;

LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180

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61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IAAVVVVALVISVCGLGVCYAORKCYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                     1 MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                         Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 298; Conservative
       metabolism.
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                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel human secreted proteins

(ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The

proteins and their coding sequences are useful for the preparation of a

diagnostic or pharmaceutical composition for diagnosting or treating a

cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,

coronary arteriosclerosis and myocardial ischaemia), neural disorders,

memune system disorders, muscular disorders, reproductive disorders,

cardiovascular disorders, pulmonary disorders, reproductive disorders,

proliferative disorders and/or cancerous diseases and conditions, for

wound healing and epithelial cell proliferation, to treat inflammation or

cinfection, for treating thrombosis and arteriosclerosis, for treating or

preventing neural damage which occurs in neuronal disorders or

controlled and prince and periodontal regeneration and aid in tissue

can be conditions such as Alzheimer's disease and parkinson's

clisease, to enhance bone and periodontal regeneration and aid in tissue

cransplants or bone grafte, to prevent skin aging or hair loss, to

marrow cells when used in combination with other cyclokines, to maintain

construction and aid or maintain and aid or maintain

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                                                                         LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
                                                                                                                                                                            LGSQSTNSSYTMNTKTGTLQPNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
                                             LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                                  Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
                                                                                                                                                                                                                                        IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; SEQ ID 817; 1881pp; English
                                                                                                                                                                                                                                                                                                                                                                                                           ABR47926 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein, SEQ ID 817,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2002; 2002WO-US09785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-277340P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-129429/12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200295010-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR47926;
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Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; rheumatoid arthritis; diabetes mellitus; hematopoletic disorder; inflammatory condition; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; halvenier's disease; cardiovascular disorder; parkinson's disease; blood-related disorder; thrombosis; atherosclerosis; blood-related disorder; thrombosis; atherosclerosis; phyperproliferative disorder; acte glomerulonephritis; Addison's disease; endocrine disorder; liver disease; reproductive system disorder; endocrine disorder; and disease; reproductive system disorder; endometriosis; inver disease; pancreatic disorder; vaccine; body height; hair colour; human.
Human secreted protein gene 25, protein.
                                                                                    ABU64994 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          970S-040762P.
970S-048100P.
970S-048189P.
970S-048357P.
970S-050934P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2001; 2001US-0852797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-040710P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-057765P
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002172994-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                15-MAY-2003
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30-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-1997
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05-SEP-1997
                                                                                                                  ABU64994;
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organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or

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The invention relates to an isolated polypeptide comprising an amino acid sequence at least 95% identical to sequence of 28 human secreted form, cargence, their fragment, polypeptide domain, epitope, secreted form, variant, allelic variant, polypeptide domain, epitope, secreted form, concluded an ATCC 9721 and 97922. Also included are the encoding encoding the proteins and mucleic acids are useful for disquosing, prognosing or amaliorating a medical condition e.g. treating, prognosing or amaliorating a medical condition of sectors is autoimmune thyroidities, autoimmune thyroidities, autoimmune thyroidities, autoimmune thyroidities, antical manatory bowel disease, disease, habetes shock, sepsias, repertusion injury, inflammatory conditions (e.g. septic shock, cepsis, recental nervous system (CNS) disorders (e.g. septic brain injury and/or stroke traumatic brain injury), neurodegenerative constraint and prior disease, and alsorders (e.g. technic and prior disease), cardiovascular disease, and cardiopulmonary processis, myocarditis, cardiovascular disease, and spease on percentic disorders (e.g. endomenties, general processis, myocarditis, deradions arterial thrombosis, for myocarditis, sarcoidosis, dermatitis, allogenic transplant rejection), hyperpituitarism), liver diseases and disorders (e.g. and pancreatic disorders (e.g. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human secreted polypeptides and polynucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of therapeutic use
                                                                                                                                                                                                                                                                                                                                                       Li Y, Zeng Z, Kyaw H, Fischer CL, Li B
Wei Y, Moore PA, Young PE, Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 186; 209pp; English.
 19-DEC-1997; 97US-068368P.
02-FEB-2001; 2001US-265583P.
12-MAR-1998; 98WO-US04858.
                                                     98US-0152060
                                                                                                                                                                                                                                                                                                                                                         Rosen CA,
Gentz RL,
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                                                                                                                                                                             FISCHER C L
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WEI Y.
MOORE P A.
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SOPPET D R.
                                                                                      RUBEN S M.
ROSEN C A.
                                                                                                                                                                                                                                                                                                     GREENE J M
                                                                                                                                          ZENG Z.
KYAW H.
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABX96990
                                                     11-SEP-1998;
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Soppet DR,
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Ferrie AM
                                                                                      (RUBE/)
(ROSE/)
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(SOPP/)
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                                                                                                                                                                                     61 LEWKKIGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGON 120
                                                                                                                                                                                                                                                 LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                                                                           LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oseophagus; stomach; small intestine; large intestine; liver; biliary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunosuppressive; vulnerary; chromosome 21q21.2.
                                                                                                                                                                                                                                                                                                                                                                      ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode.
                                                                                                                                          1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers
                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human gene 162 encoded secreted protein HTEEB42, SEQ ID NO:461.
                                                             Length 298;
                                                                                           Indels
                                                         99.7%; Score 1517; DB 24;
100.0%; Pred. No. 1.4e-118;
ive 0; Mismatches 0;
represents a secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR00172 standard; Protein; 298 AA
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                        Matches 298; Conservative
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                                                                           Best Local Similarity
                                298 AA;
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                                Sequence
                                                             Query Match
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30-JAN-2003
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CC invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening, and recombinant corrected proteins in drug screening, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein acityity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, cespohagus, stomach, small include cancers of these organs and tissues. The tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the treatment of immune disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute blological samples, as hybridisation probes, and secreted protein of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute construction may be used for chromosome and maxers. The present sequence represents a human secreted protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene therapy; extracellular region; junctional adhesion molecules;
huJAM; immune system disorder; immune deficiency; autoimmune disorder;
inflammatory disorder; cancer; wound healing; cardiovascular disease;
full-length membrane-bound huJAM protein.
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/note= "Extracellular domain; Specifically claimed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.7%; Score 1517; DB 24; Length 298; 100.0%; Pred. No. 1.4e-118; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human junctional adhesion molecule 2 (huJAM2).
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO16452 standard; protein; 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
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AC AAO1
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KW HUME
XW HUME
XM HUM
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The invention comprises the DNA and protein sequences of the extracellular region of human junctional adhesion molecules (huJAM). The extracellular huJAM DNA and protein sequences are useful in the treatment of: immune system disorders (e.g. immune deficiency); autoimmune disorders; inflammatory disorders; cancer; wound healing; or a cardiovascular disease. The present amino acid sequence represents the full-length membrane-bound huJAM2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MARRSRHRFLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                                                                                                                                                                                                                                                                                                      New extracellular human junctional adhesion molecule (huJAM)
polypeptide, useful for treating an immune system disorder such as an
immune deficiency or an inflammatory disorder, cancer, wound healing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLN1SGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.5%; Score 1514; DB 24;
99.0%; Pred. No. 2.4e-118;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human EST encoded protein SEQ ID NO: 1218.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM23693 standard, Protein; 303
                                                                                                                                                                                                                                                                                                                                                                                    or a cardiovascular disease
05-JUL-2002; 2002WO-US19800.
                                             16-JUL-2001; 2001US-305752P. 05-FEB-2002; 2002US-354345P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                        (ELIL ) LILLY & CO ELI.
                                                                                                                                                                           Heuer JG, Smith RC,
                                                                                                                                                                                                                           WPI; 2003-221848/21.
N-PSDB; AAL51599.
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Human PRO245 protein.
                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                                                                                                                                                                                                                                Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                           Asundi V:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.8%; Score 1502.5; DB 2
97.4%; Pred. No. 2.3e-117;
iive 1; Mismatches 2;
                                                                                                                                                                                                          Wang Z,
                                                                                                                                                                                                                        Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 878-879; 1275pp; English.
                                                                                                                                                                                                           Qian XB,
                                                                                                    25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                        25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                                           Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein of the invention.
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                                                                                                                                                                                                        Tang YT, Liu C, Zho
Cao Y, Drmanac RA,
                                                                                                                                                                                                                                                      2001-476164/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 AA;
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              WO200154477-A2
                                           02-AUG-2001
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AAY08060 standard; Protein; 312 AA.

11-SEP-2000 (first entry)

AAY08060;

SAXAXEX

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This invention describes a novel composition containing (apart from a carrier or excipient), a novel PRO245 polypeptide (I), its agonist or antagonist, or their fragments, for modulating: (i) infiltration of inflammatory cells into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects of inflammatory cells into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects of inflammane and anti-diabetic activity. (I), and its (ant) agonists and their fragments, are used to treat immune-related diseases, particularly T cell-mediated diseases. The diseases treated include systemic lupus erythematosus, rheumatorid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Slogreni annume-mediated thrombocytopenia (idiopathic thrombocytopenic hemoglobinuria), autoimmune thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis, diabetes mellitus, immune-mediated renal disease

CC thyroiditis), diabetes mellitus, immune-mediated renal disease

CC dlomerulonephritis, tubulointerstitial nephritis), multiple sclerosis, idiopathic demyelinating polyneuropathy, infectious hepatitis

CC inflammatory demyelinating polyneuropathy, infectious hepatitis

CHOMERIES, and sclerosing cholangitis, inflammatory bowel disease

CC ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and wiliples diseases and enterone entimune-mediated skin disease including
                                      Inflammatory cell infiltration; immune response; T cell proliferation; anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory wopathy; hemolytic nemmia; thrombocytopenia; thyroidits; diabetes mellitus; demyelinating polymeuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; skin disease; dermatitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersenstituity; urticaria; eosinophilic pneumonia; transplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, and transplantation associated diseases (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists or fragment can also be used as an adjuvant in treatment of tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition containing novel polypeptide PRO245, its agonist or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0059263.
97US-0063550.
97US-0065186.
97US-0066364.
97US-0066770.
98US-0088026.
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arthritis, spondyloarthropathies, systemic sclerosis, scleroderma, idiopathic inflammatory myopathies, dernatomyositis, polymyositis, signern's syndrome, systemic vaculitis, sarcoidosis, autoimmune hemolytic anemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria, autoimmune thrombocytopenia, thrombocytopenic purpura, immune-mediated thrombocytopenia, thyroiditis, drave's disease, immune-mediated thrombocytopenia, thyroiditis, dernyla arcophic thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis, diabetes mellitus, immune-mediated renal disease, cf the central and peripheral nervous systems such as multiple sclerosis, of the central and peripheral nervous systems such as multiple sclerosis, idiopathic polyneuropathy, hepatobiliary diseases, infectious hepatitis, hepaticis, primary bilary cirrosis, autoimmune chronic accive hepatitis, inflammatory and fibrotic lung diseases, gluten-sensitive cholangitis, inflammatory and fibrotic lung diseases, gluten-sensitive diseases allergic diseases, autoimmune or immune-mediated skin clisopathic pulmonary fibrosis and hypersensitivity pneumonitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein, transmembrane protein, human, enterocolitis, Zollinger-Ellison syndrome; gastrointestinal ulceration, congenital microvillus arrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alz; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
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Pred. No. 3.2e-114;
0; Mismatches 2;
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Best Local Similarity 99.3%;
Matches 286; Conservative
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                                                                                                                                                       1 MARRSRHRLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                                                                                                                                                                                    1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
                                                                                                                                                                                                                                                                                                                                   LGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
Antibodies against (I) can also be used for diagnosing such diseases. This sequence represents the human PRO245 protein described in the invention.
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                                                                                             Score 1465; DB 20;
Pred. No. 3.2e-114;
0; Mismatches 2;
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97US-0066364.
98US-0078936.
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Best Local Similarity 99.3%;
Matches 286; Conservative
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N-PSDB; AAX81770.
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Tumas D, Wood WI;
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Gaps

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Indels

Length 312;

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180

240

240

cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease. Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tunor drugs. PRO369 any be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

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Sequence 312 AA;

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970S-0062125
970S-0062285.
970S-0062814.
970S-0062816.
970S-0063120.
970S-0063121.
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(GETH) GENENTECH INC

Wood WI, Goddard A, Gurney AL, Pennica D, WPI; 1999-229533/19 Chen J,

N-PSDB; AAX52225

New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration

Claim 12; Fig 24; 320pp; English.

AAY13144-403 represent secreted and transmembrane human proteins.
The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal leibons [e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial

02-MAR-2000; 2000WO-US05841.

14-SEP-2000.

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08-MAR-1999;

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96.3%; Score 1465; DB 20;
99.3%; Pred. No. 3.2e-114;
iive 0; Mismatches 2;
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                                     Matches 286; Conservative
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16-DEC-1999;
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16-DEC-1999;
16-DEC-1999;
10-MAR-1999;
12-MAR-1999;
12-APR-1999;
20-APR-1999;
28-APR-1999;
04-MAY-1999;
02-JUN-1999;
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(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W; Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V; Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

WPI; 2000-572271/53. N-PSDB; AAC58586.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus

Claim 33; Fig 16; 309pp; English

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, sograthis, idiopathic inflammatory myopathies, Sograths systemic sclerosis, idiopathic inflammatory myopathies, Sograths systemic vasculitis, arcoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune con immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated ARCS8739 to ARCS8739 to ARCS8739 to ARCS873 propresent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACS8579 to ARCS842 and sequences and protein sequences given in the exemplification of the present invention.

Score 1465; DB 21 Pred. No. 3.2e-114 0; Mismatches 2	ALGYHKAYGFSAPKDQ		QGDFKNRAEMIDFNIR	QGDFKNRAEMIDFNIR	EVPSSALSGTWVELRC	EVPSSALSGTVVELRC	OFNTVSKLDTGEYSCE	QFNTVSKLDTGEYSCE	YAQRKGYFSKETSFOK	YAQRKGYFSKETSFQK
96.3%; ilarity 99.3%; Conservative	RRSRHRLLLLLLRYLVV	RRSRHRLLLLLLRYLVV	WKKLGRSVSFVYYQOTL	WKKLGRSVSFVYYQQTL	EDTVTLEVLVAPAVPSC	EDTVTLEVLVAPAVPSC	SOSTNSSYTMUTKTGTL	SQSTNSSYTMNTKTGTL	AVVVVALVISVCGLGVC	IAAVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSEN
lery Match st Local Sim: tches 286;	1 MA3	1 MAJ	61 LEV	61 LEV	121 LE	121 LEE	181 LGS	181 LGS	241 IAZ	241 IA
	3%; Score 1465; 3%; Pred. No. 3.2 0; Mismatches	96.3%; Score 1465; Similarity 99.3%; Pred. No. 3.2 6; Conservative 0; Mismatches MARRSHRLLLLERYLVVALGYHKAYGFSAPR	Query Match Best Local S Matches 286	Duery Match Best Local S Watches 286 1 1	Duery Match Best Local S Watches 286 1 1 61	Duery March Best Local S Matches 286 1 1 61 61 121	Duery Match Best Local S Best Local S Matches 286 1 1 61 61 121	Duery March Best Local S Best Local S Matches 286 1 1 61 61 121 121	Duery March Best Local S Best Local S Marches 286 1 1 61 61 121 121 121	Duery Match Best Local S Watches 286 1 1 61 121 121 121 181

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Sequence 76, Appli
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Sequence 28, Appli
Sequence 28, Appli
Sequence 29, Appli
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1 MARRSRHRLLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-254-465A-9
US-09-188-930-189
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US-09-462-270-2
US-09-312-283C-189
US-09-254-465A-23
US-09-254-465A-23
US-09-254-465A-24
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Maximum Match 100%
Listing first 45 summaries
                                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 2, Appli Sequence 2, Appli Sequence 23, Appl Sequence 24, Appl Sequence 26, Appl Sequence 31, Appl Sequence 31, Appl Sequence 503, Appl Sequence 503, Appl Sequence 50, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli	BB STATE OF THE ST	y occurring L-amino acids	Y occurring L-amino acids Length 298; Indels 0; Gaps 0;
28 195.5 12.9 365 3 US-09-272-496-2 29 191.5 12.6 365 3 US-08-928-383B-2 30 183 12.0 249 4 US-09-36-536-42 31 183 12.0 365 3 US-08-928-383B-23 33 180 11.8 365 3 US-08-928-383B-26 34 178.5 11.7 46 4 US-09-36-107A-8 35 175.5 11.5 466 4 US-09-36-241-503 36 165.5 11.1 373 4 US-09-36-241-503 37 161.5 10.6 805 3 US-08-985-25-34 40 160.5 10.6 806 2 US-08-441-861-5 41 160.5 10.6 806 3 US-08-441-861-5 42 160.5 10.6 1367 1 US-07-947-551-6 43 160.5 10.6 1367 1 US-07-947-551-6 44 160.5 10.6 1367 1 US-07-946-507-4 45 160.5 10.6 1367 1 US-07-946-507-4 45 160.5 10.6 1367 1 US-07-96-257-517-6	ALIGNMENTS -060-76 No. 6448330 INFORMATION: ANT: Rosen et al. OF INVENTION: 28 Human Secreted Protei EPERRECE: PZ003P1.US T FILING DATE: 1998-09-11 R APPLICATION NUMBER: US/09/152,060 T RILING DATE: 1998-03-12 R APPLICATION NUMBER: 60/040,762 R APPLICATION NUMBER: 60/040,710 R FILING DATE: 1997-03-14 R APPLICATION NUMBER: 60/040,100 R FILING DATE: 1997-05-30 R APPLICATION NUMBER: 60/048,100 R PILING DATE: 1997-05-30 R APPLICATION NUMBER: 60/048,189 R FILING DATE: 1997-05-30 R APPLICATION NUMBER: 60/048,357 R FILING DATE: 1997-05-30 R APPLICATION NUMBER: 60/048,370 R FILING DATE: 1997-05-30 R APPLICATION NUMBER: 60/048,370 R APPLICATION NUMBER: 60/048,370 R FILING DATE: 1997-12-19 OF SEQ ID NOS: 118 RE: PAPEMENT OF SER EAUTIN VAY: 2.0 OF SEQ ID NOS: 118 RE: PAPEMENT OF SER EAUTIN VAY: 2.0	PERTON	റം മെ

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241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
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Patent No. 6150502
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US-09-188-930-189
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ORGANISM: Human
FEATURE:
NAME/KEY: UNSURE
LOCATION: (247)...
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Goddard, Audrey
APPLICANT: Mood, William I.
APPLICANT: Wood, William I.
APPLICANT
                                                                                                                                            LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                   LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
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99.3%; Pred. No. 1.4e-136;
live 0; Mismatches 2;
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Best Local Similarity 99.3
Matches 286; Conservative
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56 TVXSRLEWK-KLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAP 114
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION UNBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 189
LENGTH: 299
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28.2%; Score 429; DB 3; Length 29
Best Local Similarity 34.2%; Pred. No. 2.7e-34;
Matches 106; Conservative 50; Mismatches 126; Indels
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LLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGK-RMQVD 233
                                                                                                                                                                                                                        234 DLNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKA----TTMSEN 288
             ----RVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVS-- 112
                                                      115 SEQGONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIR 174
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PRIOR PLING DATE: 1999-03-05
PRIOR FILING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PLING DATE: 1997-11-21
PRIOR PLING DATE: 1997-11-21
PRIOR PLING DATE: 1997-11-21
PRIOR PRING DATE: 1998-09-17
PRIOR PILING DATE: 1998-09-17
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CURRENT FILING DATE: 1999-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09254465A Patent No. 6410708 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genentech, Inc.
Ashkenazi, Avi J.
Fong, Sherman
Goddard, Audrey
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Best Local Similarity 34.2<sup>†</sup>
Matches 106; Conservative
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290 EFKQTSSFLV 299
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APPLICANT: SmithKline Beecham Corporation

TITLE OF INVENTION: Human F11 Antigen: A Cell Surface

TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
FILE REFERENCE: GH-7015004

CURRENT APPLICATION NUMBER: US/09/462,270

CURRENT FILING DATE: 2000-01-05

PRIOR FILING DATE: 1997-07-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011.cd CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SOFFWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 331
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Best Local Similarity 34.24
Matches 106; Conservative
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Matches 106; Conservative
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290 EFKQTSSFLV 299
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US-09-462-270-2
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FNGTH: 299
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.2%; Score 429; DB 4; Length 299; 34.2%; Pred. No. 2.7e-34; ive 50; Mismatches 126; Indels
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Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Mateson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
                                                                                                                                                                 Sequence 189, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
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Matches 106, Conservative
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290 EFKQTSSFLV 299
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EFKQTSSFLV 299
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ORGANISM: Mouse
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US-09-312-283C-331
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APPLICANT: FONG, Sherman
APPLICANT: Gordard, Audrey
APPLICANT: Gordard, Audrey
APPLICANT: Gordard, Audrey
APPLICANT: Gordard, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION OF DISEASES
FRICA REPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1999-11-21
PRIOR PELICATION NUMBER: US 60/066,364
PRIOR PELICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-17
PRIOR FILING DATE: 1998-03-17
PRIOR FILING DATE: 1998-09-17
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TITLE OF INVENTION: and Methods for Their Use FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 331
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Patent No. 6410708
GENERAL INFORMATION:
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Ashkenazi, Avi J.
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Matches 106; Conservative
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290 EFKQTSSFLV 299
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                             US-09-312-283C-331
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US-09-254-465A-10
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## APPLICANT: ABDREHBZ1, AV1 U.

APPLICANT: FONGY, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Unmas, Daniel

APPLICANT: Wood, William I.

TILLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS

FILE REFERENCE: P1216R1(US)

FILE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS

FILE REFERENCE: 1999-03-05

FILE REPERENCE: 1999-03-05

FRIOR FILING DATE: 1998-11-20

FRIOR APPLICATION NUMBER: US 60/066,364

FRIOR APPLICATION NUMBER: US 60/066,364

FRIOR PRICH FILING DATE: 1998-03-20

FRIOR PRICH PRICH NUMBER: US 60/078,936

FRIOR FILING DATE: 1998-03-20

FRIOR FILING DATE: 1998-03-20

FRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 30

**SEQ ID NO 25**

**TOWNEY: NUMBER OF SEQ ID NO
61 EDRVTFLPTGITFKSVTREDTGTYTCMVS--EEGGNSYGEVKVKLIVLVPPSKPTVNIPS 118
                                                                                                                         204 VSKLDTGEYSCEARNSVGYRRCPGK-RMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 262
                                                                                                                                                                                                                                                                     84 KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 EDRUTFLPTGITFKSVTREDIGTYTCMVS--EEGGNSYGEVKVKLIVLVPPSKPTVNIPS 121
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                                                                          144 SALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNT
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239 SRGHFDR----TKKGTSSKKVIYSQ 259
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Sequence 25, Application US/09254465A; Patent No. 641070B; Patent INFORMATION:
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Ashkenazi, Avi J.
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APPLICANT: Abkenazi, Avi J.
APPLICANT: Abkenazi, Avi J.
APPLICANT: Abkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Wood, William I.
APPLICANT: Wood William II.
APPLICANT: Wood William II.
APPLICANT: Wood William III.
APPLICANT: Wood William III.
APPLICANT: Wood William III.
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                                                                                                                                                                                                                                                                                                                            64 KKL-GRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 SQS-TNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNSVG-YRRCPGKRMQVDDLNISGI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 IAAVVVVALVISVCGLGVCYAQRKGYF---SKETSFQKSNSSSKATTMSENDFKHTKSFI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEW
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                                                                                                             Gaps
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                               Query Match
27.7%; Score 421; DB 4; Length 300;
Best Local Similarity 34.6%; Pred. No. 1.7e-33;
Matches 104; Conservative 55; Mismatches 130; Indels 12;
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ORGANISM: Homo sapiens
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LENGTH: 260
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US-09-254-465A-24
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Goddard, Austin L.
APPLICANT: Tumas, Daniel
AAPPLICANT: Tumas, Daniel
AAPPLICANT: Wood, William I.
TITLE OF INVENTION: OF DISBASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISBASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISBASES CHARACTERIZED BY A33- RELATED ANTIGENS
CURRENT ELLING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-11-21
PRIOR FILING DATE: 1999-11-21
PRIOR FILING DATE: 1999-11-21
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 24
BENGTH: 270
TWORD: DATE: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 TVXSRLEWK-KLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 ----RVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVS-- 112
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APPLICANT: SmithKline Beecham Corporation
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Human F11 Antigen: A Cell Surface
TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
FILE REFERENCE: GH-70150US
CURRENT APPLICATION NUMBER: US/09/462,270
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/052,186
PRIOR APPLICATION NUMBER: 60/052,186
NUMBER OF SEG ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 205;
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; Sequence 24, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
                                 Sequence 4, Application US/09462270
Patent No. 6358707
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Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: HOMO SAPIENS
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          LENGTH: 205
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### APPLICANT: Genentech, Inc.
### APPLICANT: Genentech, Inc.
### APPLICANT: Genentech, Inc.
### APPLICANT: Goddard, Audrey.
### APPLICANT: Goddard, Audrey.
### APPLICANT: Goddard, Audrey.
### APPLICANT: Mapier, Mary A.
### APPLICANT: Mood, William I.
### APPLICANT: Wood, William I.
### APPLICANT: WOOD OF BISEASES CHARACTERIZED BY A33-RELATED ANTIGENS
### APPLICANT: PALOR DATE: 1999-03-05
### PRIOR PRILING DATE: 1999-11-20
### PRIOR APPLICANT: WUMBER: US 60/078,936
### PRIOR APPLICANT: WUMBER: US 60/078,936
### PRIOR APPLICANT: WUMBER: PCT/US98/19437
### PRIOR PILING DATE: 1999-09-17
### WUMBER OF SEQ ID NOS: 30
### APPLICANT: WUMBER: US 60/078,936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 IVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 TWNTKTGTLOFNTVSKLDTGEYSCEARNSVGYRRCP-GKRMQVDDLNIS-----GIIA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 LKNISTDT------SGYXICTSSNEEGTQFCNITVAVRSPSMNVALYVGIAVGVVA 233
                                                                                                                                                                                                                                                        131 LVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSY 190
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                                                                                                                                                                                                                                                                                                                                                                            81 GD-FKNR-----AEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDT---VTLEV
                                                                                                                                                                                        30 SAPKDQQVVTAVXYQEAILACKTPKKTVXSR---LEWKKL-----GRSVSFVYYQQT-LQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97; Indels 42; Gaps
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15.2%; Score 231; DB 4; Length 273;
Best Local Similarity 28.6%; Pred. No. 8.6e-15;
Matches 72; Conservative 41; Mismatches 97; Indels ;
              Length 270;
15.2%; Score 231; DB 4; Length 270
28.6%; Pred. No. 8.4e-15;
ive 41; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 26, Application US/09254465A; Patent No. 6410708
                                                                                                 72; Conservative
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ORGANISM: Homo sapiens
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-08-597-495B-22

Sequence 22, Application US/08597495B

Sequence 22, Application US/08597495B

Patent No. 5712369

GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gard;

APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;

APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;

APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron

TITLE OF INVENTION: Colon Cell And Colon Cancer Cell

TITLE OF INVENTION: Associated Nucleic Acid Molecules, Frotein And Peptides

NUMBER OF SEQUENCES: 29

CORRESPONDENCE SAPERS: Relfe & Lynch

STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97; Indels 42; Gaps 11;
                                                                                          191 TMNTKTGTLOFNTVSKLDTGEYSCEARNSVGYRRCP-GKRMQVDDLNIS-----GIIA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 GD-FKNR-----AEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDT---VTLEV 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 SAPKDQQVVTAVXYQEAILACKTPKKTVXSR---LEWKKL-----GRSySFVXYQQT-LQ 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 5712369man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5316.1
TELECOMINICATION INFORMATION:
TELEPRONE: (212) 688-9200
FELEPRONE: (212) 688-9200
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,495B
FILING DATE: 02-Feb-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 amino acids
                                                                                                                                                     243 AVVVVALVISVC 254
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237 ALIIIGIIIYCC 248
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Matches 72; Conservative
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Sequence 38, Appl Sequence 2, Appl Sequence 2, Appli Sequence 76, Appl Sequence 76, Appl Sequence 64, 
                                                                                                                                                                                   9, 2003, 17:13:07 ; Search time 27.5157 Seconds (without alignments) 2014.238 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                     1521
1 MARRSRHRLLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-799-777-30
S US-10-139-849-2
S US-10-132-791-2
US-09-853-161-76
US-09-852-65,00-76
US-09-905-320-64
US-09-905-320-64
US-09-905-320-64
US-09-905-320-64
US-09-905-320-64
US-09-905-853-64
US-09-907-841-64
US-09-907-841-64
US-09-907-841-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  684280 seqs, 185983659 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                          US-09-852-797-76
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Match Length
                                                                                                                                                                                             December
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999.8
999.7
996.3
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16	1465	6.3	312	11	-906-60-	Seguence 6	
17	1465	96.3	312	11			
18	1465	96.3	312	11	-09-907		
19	1465	96.3	312	11	-09	Sequence 6	
20	1465	96.3	312	11	US-09-904-859-64		
21	1465	ė.	312	11	-09		
22	1465	96.3	312	11	US-09-904-820-64	Seguence 6	64, Ap
23	1465	ė.	312	11	US-09-904-786-64		
24	1465	ė.	312	11	-09		
25	1465	9	312	11	US-09-906-700-64		
56	1465	96.3	312	11	US-09-903-786-64		
27	1465	9	312	11	US-09-902-903-64		
28	1465	9	312	11	US-09-903-749A-64	Seguence 6	
29	1465	Ġ	312	11	US-09-904-119-64		
30	1465	96.3	312	11	US-09-904-956-64		
31	1465	Ġ.	312	11	US-09-902-736-64		
32	1465	ů.	312	11	US-09-907-794-64		
33	1465	ö	312	11	60-		_
34	1465	Ġ	312	11	-09		_
32	1465	Ġ	312	11	-09		
36	1465	Ġ	312	11	60-		
37	1465	Ġ	312	11	6		_
38	1465	96.3	312	11	6		
39	1465	Ġ	312	11			
40	1465	ö	312	11	-09-904-553		_
41	1465	Ġ	312	11	-09-905-381		
42	1465	Ġ	312	11	-09-905-088		
43	1465	Ġ	312	11	-09-907-575		
44	1465	Ġ	312	11	-09-905-075-	a	_
45	1465	'n	312	7	US-09-902-759-64	ø	4, Appl

ALIGNMENTS

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US-09-745-763-38

1 US-09-745-763-38

1 US-09-745-763-38

1 Sequence 38, Application US/09745763

2 Patent No. US20020065394A1

2 GENERAL INFORMATION:

1 LaVallie, Edward R.

1 LaVallie, Edward R.

1 LaVallie, Edward R.

2 Collins-Racie, Lisa A.

2 Evans, Cheryl
Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 219

CORRESSEE Genetics Institute, Inc.

STREET: 87 CambridgePark Drive
CITY: CambridgePark Drive
CITY: CambridgePark Drive
STREET: 87 CambridgePark Drive
COUNTRY: U.S.A.

COUNTRY: DS.A.

CONPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30

CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 41,323

TELECOMMONICATION INFORMATION:
NAME: Sprunger, Suzanne A.

REGISTRATION NUMBER: 41,323

TELEPRONE: (617) 876-5851
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61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLN1SG1 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEATLACKTPKKTVSSR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSRATTMSENDFKHTKSFII 298
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                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                               Length 298;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10139849
Publication No. US20030079238A1
GENERAL INFORMATION:
APPLICANT: Cunningham, Sonia
APPLICANT: Cunningham, Sonia
TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A PUNCTIONAL ADHESION PROTEIN
                                                                                                                                                                                                                                                                                                                                          99.8%; Score 1518; DB 9;
99.3%; Pred. No. 9.8e-136;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/643,929
FILING DATE: 23-Aug-2000
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/139,849
FILING DATE: 07-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: DUCONOTO2
CLONE: 1714050
SEQUENCE DESCRIPTION: SEQ. ID NO: 30
                       IELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60601
COMPUTER READABLE FORM:
                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                             Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: IL
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              US-09-799-777-30
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Corley, Neil C.
Guegler, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
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                                                                                                                                                                                                                                           Length 298;
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                                                                                                                                                                                                                                        Query Match 99.8%; Score 1518; DB 9;
Best Local Similarity 99.3%; Pred. No. 9.8e-136;
Matches 296; Conservative 0; Mismatches 2;
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
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MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION STROMMON
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/002,485
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INPORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
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Patent No. US20020091244A1
GENERAL INFORMATION:
                 SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
INFORMATION FOR SEQ ID NO: 38:
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STATE: CALIFORNIA
COUNTRY: USA
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US-09-799-777-30
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-853-161-76
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241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
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100.0%; Pred. No. 1.2e-135;
Live 0; Mismatches 0;
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TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P3
                                                                                                                                                                                                                                                                                                                FILE REPERENCE: PZO101973

CURRENT PILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 06/265,583

PRIOR PILING DATE: 2001-05-11

PRIOR PILING DATE: 2001-02-02

PRIOR PILING DATE: 1998-09-11

PRIOR PLING DATE: 1997-03-12

PRIOR PLING DATE: 1997-03-14

PRIOR PLING DATE: 1997-03-14

PRIOR PLING DATE: 1997-03-14

PRIOR PLING DATE: 1997-03-14

PRIOR PLING DATE: 1997-05-30

PRIOR PLING DATE: 1997-05-30
                                                                                                                                                                                         Sequence 76, Application US/09853161
Patent No. US20020076756A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 298; Conservative
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ORGANISM: Homo sapiens
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Publication No. US20030130166A1
GENERAL INFORMATION:
TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (JA FILE REFERENCE: TEX4542P0430
CURRENT PELLING DATIS: 2003-12-10
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 298
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99.3%; Pred. No. 9.8e-136;
ive 0; Mismatches 2;
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                                                                                                                                                                                                                                                       Score 1518, DB 15,
Pred. No. 9.8e-136;
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99.8%; Score 1518; D
Best Local Similarity 99.3%; Pred. No. 9.8e
Matches 296; Conservative 0; Mismatches
                                                                                    LENGTH: 298 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
TELEPHONE: 312-616-5400
                 TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Matches 296; Conservative
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US-10-192-791-2
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COTHER INFORMATION: (42)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEX: SITE
LOCATION: (58)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-852-797-76
                                       241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                               241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
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99.7%; Score 1517; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-135;
Matches 298; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 76, Application US/09852797; Patent No. US20020172994A1; GENERAL INFORMATION: ; APPLICANT: Rosen et al. TITLE OF INVENTION: 28 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE REFERENCE: 28 Human Secreted Protein PURENCE PERSONS. 28 Human Secreted Protein PERSONS. 29 CURRENT APPLICATION NUMBER: US/09/852,797 CURRENT FILING DATE: 2001-05-11 PRIOR PAPLICATION NUMBER: 09/152,060 PRIOR FILING DATE: 1998-09-11 PRIOR PLILING DATE: 1998-09-11 PRIOR PLILING DATE: 1998-09-11 PRIOR PELING DATE: 1997-03-14 PRIOR PELING DATE: 1997-05-30 PRIOR PELING DATE: 1997-06-05 PRIOR PELING DATE: 1997-06-05 PRIOR PELING DATE: 1997-06-05 PRIOR PELING DATE: 1997-06-06 PRIOR PELING DATE: 1997-01-06-06 PRIOR PELING DATE: 1997-01-10-10 PRIOR PEUDIOR DATE: 1007-10-10 PRIOR PEUDIOR PEUDIOR PEUDIOR PEUDIOR PE
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ORGANISM: Homo sapiens
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181 LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-852-659A-76
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                                                                          241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFXHTKSFII 298
                                                                                                             241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSENDFKHTKSFII 298
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US-09-852-659A-76

US-09-852-659A-76

Sequence 76, Application US/09852659A

Patent No. US20020077287A1

GENERAL INPORMATION:

TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPERBENCE: P2003P4

CURRENT APPLICATION NUMBER: US/09/852,659A

CURRENT PILING DATE: 2001-05-11

PRIOR PELICATION NUMBER: 06/25,583

PRIOR PELICATION NUMBER: 09/152,060

PRIOR FILING DATE: 1998-09-11

PRIOR PELICATION NUMBER: 06/040,762

PRIOR PELICATION NUMBER: 60/040,762

PRIOR PELING DATE: 1997-03-14

PRIOR PELING DATE: 1997-03-16

PRIOR PELING DATE: 1997-03-16

PRIOR PELING DATE: 1997-05-30

PRIOR PELING DATE: 1997-06-06

PRIOR PELING DATE: 1997-06-06-06

PRIOR PELING DATE: 1997-06-06

PRIOR PELING DATE: 1997-06-06-06

PRIOR PELING DATE: 1997-0
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NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 76
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (58)
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NAME/KEY: SITE
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APPLICANT: Tunds, Daniel, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-0.04
FRIOR PELING DATE: 2000-0.02-22
FRIOR PELING DATE: 1990-0.0-22
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR APPLICATION NUMBER: DCT/US99/2094
FRIOR PILING DATE: 1990-0.0-3
FRIOR FILING DATE: 1990-0.0-3
FRIOR FILING DATE: 1990-0.0-3
FRIOR FILING DATE: 1990-0.0-3
FRIOR FILING DATE: 1990-0.0-13
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FRIOR FILING DATE: 1990-0.0-15
FRIOR FILING DATE: 1990-0.0-15
FRIOR FILING DATE: 1990-0.0-15
FRIOR FILING DATE: 1990-0.0-15
FRIOR FILING DATE: 1990-1.0-05
FRIOR FILING DATE: 1990-1.0-05
FRIOR FILING DATE: 1990-1.0-05
FRIOR FILING DATE: 1990-1.2-02
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR FILING DATE: 1990-1.2-02
FRIOR FILING DATE: 1990-1.2-02
LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
                                    241 JAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
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Patent No. US20020132240A1
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Grimaldi, Christopher
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Filvaroff, Ellen
Fong, Sherman
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
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APPLICANT: Paoni, Micholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-11
CURRENT APPLICATION NUMBER: US/09/909,088B
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Pred. No. 1.1e-130;
0; Mismatches 2;
          PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
APPLICATION NUMBER: PCT/US99/30911
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Grimaldi, Christopher J.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gao, Wei-Qiang
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Mather, Jennie P.
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Best Local Similarity 99.37
Matches 286; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
                                                                                                                            LENGTH: 312

TYPE: PRT

CRGANISM: Homo sapiens

US-09-909-320-64
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Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
                         Desnoyers, Luc
Eaton, Dan L.
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TYPE: PRT
ORGANISM: Homo sapiens
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        PRIOR METALLICATION NUMBER: 05 00/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
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PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 
APPLICATION NUMBER: PCT/US00/04414
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Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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Best Local Similarity
Matches 286; Conserv
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    Length 312;
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  Score 1465; DB 10;
Pred. No. 1.1e-130;
0; Mismatches 2;
   96.3%;
Query Match
Best Local Similarity 99.3
Matches 286; Conservative
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MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR

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181 LGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
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241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
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PRIOR PELLOATION NUMBER: US/09/665,350
PRIOR PELLING DATE: 2000-09-18
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PELLOATION NUMBER: US 60/146,222
PRIOR PELLOATION NUMBER: US 60/146,222
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-09-09
PRIOR PELLING DATE: 1999-09-09
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21547
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PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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Godowski, Paul J.
Grimaldi, Christopher J.
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Publication No. US20020192659A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Paoni, Nicholas F.
Roy, Margaret Ann
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT: Abhkenazi, Avi J.
APPLICANT: Forg. Sherman
APPLICANT: Goddard, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Mapler, Mary A.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFERENCE: P1216R1(US)
                    61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEGQQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/953,499
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US/09/254,465
PRIOR FILING DATE: 1999-03-05
PRIOR PLING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR PILING DATE: 1998-11-21
PRIOR PILING DATE: 1998-11-21
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-05
PRIOR PILING DATE: 1998-09-07
PRIOR PILING DATE: 1998-09-17
PRIOR PILING DATE: 1998-09-17
SEQ ID NOS: 30
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; ORGANISM: Homo sapiens
US-09-953-499-9
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Pred. No. 1.1e-130;
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96.3%; Score 1465; D
Best Local Similarity 99.3%; Pred. No. 1.1e
Matches 286; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
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CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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Grimaldi, Christopher J.
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Publication No. US20020197671A1
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Pather, Jennie P.
Pan, James
Pan, James
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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                                                                                                            ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-64
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61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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Pred. No. 1.1e-130;
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
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PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-13-03
PRIOR PILING DATE: 1999-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Homo Sapien
US-09-907-824-64
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Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
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Eaton, Dan L.
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Tumas, Daniel
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Timothy A.
APPLICANT: Timothy P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11_20
FRIOR FILING DATE: 10466-14
CURRENT FILING DATE: 10460-02-26
FRIOR FILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-07-26
FRIOR PELING DATE: 1999-07-26
FRIOR PELING DATE: 1999-07-26
FRIOR PELING DATE: 1999-07-26
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FRIOR FILING DATE: 1999-10-16
FRIOR FILING DATE: 1999-10-16
FRIOR FILING DATE: 1999-10-05
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99.3%; Pred. No. 1.1e-130;
iive 0; Mismatches 2;
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                   Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                                                                              Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Desnoyers, Luc
Eaton, Dan L.
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Best Local Similarity 99.3
Matches 286; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                       Query Match 96.3%; Score 1465; DB 11; Length 312; Best Local Similarity 99.3%; Pred. No. 1.1e-130; Matches 286; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR PILING DATE: 1999-12-20
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
                                                                                                                    TYPE: PRT
CORGANISM: Homo Sapien
US-09-904-011-64
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Search completed: December 9, 2003, 17:22:01 Job time : 29.5157 secs

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GenCore version 5.1.6
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                  Copyright
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sw model using - protein search, OM protein

December Run on:

9, 2003, 17:09:51; Search time 15.0557 Seconds (without alignments) 1903.477 Million cell updates/sec

US-09-852-797-76

1521 1 MARRSRHRLLLLLLRYLVVA.....SSKATTMSENDFKHTKSFII 298 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	junctional adbasio		1	A I I	08 - DN		tyrosine	nonspecific cross-		kinase	cyte an	hymothetical prote	1 5	π			hypotherical prote		١.	cell adhesion prot	neural cell adheai	Drotein-tvrogine-n	Drotein-tvrogine-n	leukocyte antigen-	hiliary alvoorote	Drotein-tyroeine-n	protein cyroning proping	hynotherical prote	ecto-ATPase precur
SUMMARIES	O.	S56749	JC7780	A41054	B41054	T29757	138346	A41228	A27681	JC5702	JC5701	TDHULK	T23007	T34416	JE0100	JC5700	JC1508	T46283	T20992	T43290	S19247	JN0635	158148	846217	S46216	S34338	150212	\$50893	T33433	47
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	Length	299	365	811	873	6642	7962	1367	344	860	868	1897	1328	2783	725	850	521	773	5175	5198	1033	1092	1501	1863	1898	521	1499	1907	352	519
de	Query Match	28.2	•	12.2	٠			10.6	•		10.3				10.2		10.1	•	10.0				9.9				٠.		8.6	
	Score	429	201.5	186	186	171	163.5	160.5	157	157	157	156	155.5	155.5	155	155	153.5	152	152	152	151.5	151	151	151	151	150.5	150	150	149.5	48.
	Result No.		7	Э	4	Ω	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

neural cell adhesi	neural cell adhesi	cell	cell	protein-tyrosine-p	connectin/titin -	biliary glycoprote	transmembrane carc	biliary glycoprote	biliary glycoprote	neural cell adhesi	kinase-like protei	dutt1 protein - mo	transmembrane rece	amalgam protein pr	irregular chiasm C
JE0099	IJXLNL	T30532	IJCHNL	A56178	T42633	JH0394	C30127	A32164	WMMSR1	IJHUNG	A39712	T30805	T14160	A31923	A49448
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72	108	127	109	191	416	41	46	25	456	761	1051	161	16	33	76
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9.7	_	6.7	9.7	9.7	9.7	9.7	7.6	9.7	9.6		9.6	9.6	9.6	9.5	9.5

ALIGNMENTS

1		
ESULT	56749	

junctional adhesion molecule precursor - human
N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C;Species: Homo sapiens (man)
C;Species: Broocasion: A559406; S56749
R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; My Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut: A;Reference number: A59406; MUID:99323940; PMID:10395639

A;Status: preliminary
A;Molecule type: DNA
B;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem J. 310, 155-162, 1995
Biochem J. 310, 155-199
Biochem J. 310, 155-

A,Gene: JAM C,Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet C;Keywords: signal sequence #status predicted <SIG> F;1-25/Domain: signal sequence #status predicted <MAT>

membrane

Gaps Query Match 28.2%; Score 429; DB 2; Length 299; Best Local Similarity 34.2%; Pred. No. 5.2e-27; Matches 106; Conservative 50; Mismatches 126; Indels 28;

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56 TVXSRLEWK-KLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAP 114 ઠે

112 셤

SEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIR 174 113 EEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIV 172 115 ò 셤

175 ઠે

LLENPRLGSOSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGK-RMQVD 233 අ

234 DINISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKA----TTMSEN 288 ..

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us-09-852-797-76.rpr

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Query Match
Best Local Similarity 24.6%
Matches 67; Conservative
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C;Genetics:
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A'Molecule type: mRNA
A'Residues: 1-873 <GRE>
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                                                                                                                                                                            coxsackie- and adenovirus receptor - bovine (5)pecies: Bos primigenius taurus (cattle) (5)pecies: Bos primigenius taurus (cattle) (5)pecies: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002 (5)Accession: JC7780 #Sequence_traindberg, M.; Van Ranst, M. Biochem. Biophys Res. Commun. 288, 805-808, 2001 A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor A;Reference number: JC7780 A;Accession: JC7780
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AY033651
C;Comment: This protein serves as the primary adenoviral attachment site on bovine celle
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C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C; Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C; Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
B; Grosephion A41054
Cell 67, 45-57, 1991
A; Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A; Printer C analysis of growth Cone guidance in Drosophila: fasciclin II functions
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C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YRCEV-SAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEWQK-----LSDSQKLPTSWLPEMTSPVISVKNASAEYSGTYTCTVRNRVGSDQC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 LLRLDVVPPSNRAGTIAGAVIGTLLALVLIALIVFCCH----KKRREEKYEKEVHHDIRE 279
  ERNVGVIVAAVLVTLILLGILVFGIWFAYSRGHFDRT----KKGTSSKKVIYSQPSARSEG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 DNOKVDOVIILYSGDKIYDDYYQ-----DLKGRVHFTSNDLKSGDASINVTNLQLSDIGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQ--- 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LILIRFILLCGVADFTRGLSITTPEQMIEKAKGETÄYLPCKFTLGPEDQGPLDIEWLLSPA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 LLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACK---TPKKTVXSRLEW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:9157403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GRSVSFVYYQQTLQGDFKNRAEMI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.2%; Score 201.5; DB 2
llarity 24.5%; Pred. No. 1.2e-08;
Conservative 46; Mismatches 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Cross-references: GB:M77165; NID:g157402; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KSNSSSKATTMSEN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 DVPPPKSRTSTARSYIGSN 298
                                        DFKHTKSFII 298
                                                                    EFKQTSSFLV 299
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-365 <THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-811 <GRE>
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                                        289
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C;Species: Drosophila melanogaster
C;Abate: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C;Accession: B41054
R;Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A;Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A;Reference number: A41054; MUID:92005695; PMID:1913818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: FlyBase:FBgn0000635
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm:
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fasciclin II PI-linked splice form precursor - fruit fly (Drosophila melanogaster)
                                                                13;
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                                                                                                                                                                                                                                                                                  240 EAVEGKPFAANCTAR-GKPVPEISWIRDATQL-----NVATADRFQVNPQTGLVTISS 291
                                                                                                                                                                                                                                                  84 KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 143
                                                                                                                                                                                                                                                                                                                                                                             144 SALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSKLDTGEYSCEARNSVGYRRCPGK-----RMQVDDL-NISGIIAAVVVVALVISVCGLG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 VSQDDYGTYTCLAKNRAGVVDQKTKLNVLVRPQIYELYNVTGARTKEIAI------ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341
                                                                                                                          30 SAPKDQQVVTAVXYQEA1LACKT---PKKTVXSRLEWKKLG---RSVSFVYYQQTLQGDF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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                                                                Gaps
                                                                                                                                                                 54;
   Length 811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 873;
12.2%; Score 186; DB 2; Length 81 24.6%; Pred. No. 5.5e-07; ive 50; Mismatches 101; Indels
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Best Local Similarity 24.6%; Pred. No. 6e-07;
Matches 67; Conservative 50; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 VCYAQRKGYFSKETSFQKSNSSSKATTMSEND 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCRA--KGRPAPAITFRRWGTQEEYTNGQQDD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 VCYAQRKGYFSKETSFQKSNSSSKATTMSEND 289
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215 EARNSVG
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                C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C;Accession: T2979;
R;Du, Z; Le, T.T.; Wilson, R.
Submitted to the EMBL Data Library, May 1997
A;Reference number: Z20679
A;Residues: 1-6642 <DUZ>
A;Residues: 1-6642 <DUZ>
A;Residues: 1-6642 <DUZ>
A;Residues: BMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CESP:unc-89
A;Reperimental source: strain Bristol N2; clone C09D1
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 1
A;Introns: 17/2; 108/3; 6153/2; 6515/1; 6552/3; 6609/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glastic titin - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Solwers: B.
Schence 270, 231-256, 1995
R.Labeit, S.; Kolmerer, B.
Schence 270, 231-256, 1995
A.Title: Titins: glant proteins in charge of muscle ultrastructure and elasticity.
A.Rocession: 138346
A.Title: Titins: A.Title: A.Molecula trians: A.Title: Titins and Elasticity.
A.Accession: 138346
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Nolecula type: mRNA
A.Residues: 1-7962 - RES.
A.Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3823 GRGAPEFVELLRSCTVTEKQQAILKCKV-KGEPRPKIKWTKEGKEVEM-----SAR 3872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3873 VRAEHKDDGTLTLTFDNVTQADAGEYRCE--AENEYGSAWTEGPIIVTLEGAPKIDG-EA 3929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-----SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 VTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEV----PSSALSGTVVELR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAILACKTPKKTVXSRLEWKKLGRSV-----SFVYYQQTLQGDFKNRAEMIDFNIRIKN 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 GFSAPKDQQVV---TAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 NSSYTMNTKTGTLQFN-TVSKL-DTGEYSCEARNSVG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 10.7%; Score 163.5; DB 2; 1 Similarity 28.3%; Pred. No. 0.00053; 53; Conservative 30; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 171; DB 2; 28.1%; Pred. No. 0.00011; ive 29; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
protein UNC-89 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 2q31-2q31
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Matches 61; Conserv
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Best Local S
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C;Species: Mus musculus (house mouse)
C;Date: 19-Jun-1992 #sequence revision 19-Jun-1992 #text_change 04-Feb-2000
C;Date: 19-Jun-1992 #sequence revision 19-Jun-1992 #text_change 04-Feb-2000
C;Date: 19-Jun-1992 #sequence revision 19-Jun-1993
R;Accession: A41228; A6605; IS8855; S18812, S29991
R;Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R. Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
A;Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitial;Reference number: A41228; MUID:92020984; PMID:1171995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: prefininary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: Third canna
A;Molecule type: Third canna
A;Cross-references: GB:X55397; NID:g50976; PIDN:CAA42040.1; PID:g50977
B;Millauer, B.; Mizigmann-Voos, S.; Schnurch, H.; Martinez, R.; Moller, N.P.; Risau, W.
B;Millauer, B.; Mizigmann-Voos, S.; Schnurch, H.; Martinez, R.; Moller, N.P.; Risau, W.
A;Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a maj
A;Reference number: A46065; MUID:93208880; PMID:7681362
A;Accession: A46065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Note: submitted to the EMBL Data Library, January 1993
A;Note: sequence extracted from NCBI backbone (NCBIP:128064)
B;Oelrichs, R.B.; Reid, H.H.; Bernard, O.; Ziemiecki, A.; Wilks, A.F.
Oncogene 8, 11-18, 1993
A;Title: NYK/Fix-1: a putative receptor protein tyrosine kinase isolated from E10 embry
A;Reference number: 158365; MUID:93141255; PMID:8423988
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-679, 'D',680-1340, 'RSPPV' <OEL>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: FLK-1; NYK
S;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane
F;830-1165/Domain: protein kinase homology <KIN>
F;838-846/Region: protein kinase ATP-binding motif
                                                   ----EVSAPSEOGONLEEDTVTLEV 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 LVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 TMNTKTGTLOFNTVSKLDTGEYSCEARNSVGYRR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 ---IRIKNVTRSDAGKYRC------
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2817 KAENSIG 2823
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A;Note: the list of introns may be incomplete C;Superfamily: carcinoembryonic antigen precursor amino-termi C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen; carcinoembryonic antigen; lipoprotein; membrane protein; phosphat F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN> F;1-34/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;304,111,115,152,173,197,224,256,274,288,292/Banding site: carbohydrate (Asn) (covalen F;309/Binding site: carbohydrate (Asn) (covalent) #status predicted F;3109/Binding site: Garbohydrate (Asn) (covalent) #status predicted F;320/Modified site: GPI-anchor ethanolamina amidated carboxyl end (Gly) (in mature for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
C;Dates: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
C;Accession: JCS702; PCF417
R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miya J. Blochem. 122, 675-680, 1997
A;Title: A novel brain-derived member of the epidermal growth factor family that inters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown
A;Reatus: nucleic acid sequence not shown
A;Reatdues: 'F',212-213,223-860 <HIZ>
A;Reatdues: 'F',212-213,223-860 <HIZ>
A;Cross-references: DDBJAB001576; NID:g2605478; PIDN:BAA23348.1; PID:g2605479
A;Experimental source: PC-12 cell
C;Comment: This protein is a member of the epidermal growth factor family. It is functiating the differentiation of MDA-MB-453 cells.
C;Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; immun
                                                                                                                                                                                                                                   AjStatus: preliminary; not compared with conceptual translation
AjMolecule type: DNA
Asesidues: 35-137 'L',139-141 «KH2»
CjComment: This protein appears to be processed at the carboxyl terminus and anchored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMTLTLLSVKRNDAGSYEČEIQNPASANRS---DPVTLNVLYGPDGPTIS-PSKANYRPG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 TVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TFQQSTQELFIPNITVNN 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ErbB kinase activator alpha2a, brain and thymus - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Nov_1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-34/Domain: signal sequence #status predicted <SIG>
5;35-320/Product: nonspecific cross-reacting antigen #status experimental
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
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A;Accession: JC5702
A;Status: nucleic acid sequence not shown
A;Molecule trune: mpun
number: A44476; MUID:93052339; PMID:1427854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.3%; Score 157; DB 2;
Best Local Similarity 28.4%; Pred. No. 4.2e-05;
Matches 48; Conservative 25; Mismatches 62;
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F;361-397/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: GDB:120221; OMIM:163980
A, Map position: 19q13.2-19q13.2
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                                                                                                               A; Molecule type: DNA
A; Residues: 35-141 < KHA>
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A; Residues: 1-860 < HIG>
                                                                                                                                                                                                  A; Accession: F44476
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: NCA
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                                             Name of the cross-reacting antigen precursor - human nampeoffic cross-reacting antigen precursor - human nampeoffic cross-reacting antigen precursor - human cannot be considered above and the construction of the construction o
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A; Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194,204-224;233-308;310
B; Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A; Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A; Reference number: A26414; MUID:87147209; PMID:3469650
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A;Residues: 35-69 <-pax>
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem,
Genomics 14, 384-390, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: C26414
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A;Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region ht A;Areference number: JL0051; MUID:89035978; PMID:2972792 A;Accession: 803841 A;Accession: 803841 A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
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C,Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fi39-199/Domain: immunoglobulin nomology <IPM12>
Fi39-199/Domain: immunoglobulin nomology <IPM12>
Fi30-290/Domain: immunoglobulin homology <IPM13>
Fi306-290/Domain: immunoglobulin homology <IPM13>
Fi306-290/Domain: ibronectin type III repeat homology <FN3A>
Fi301-389/Domain: fibronectin type III repeat homology <FN3D>
Fi501-583/Domain: fibronectin type III repeat homology <FN3D>
Fi508-789/Domain: fibronectin type III repeat homology <FN3D>
Fi508-789/Domain: fibronectin type III repeat homology <FN3D>
Fi508-789/Domain: fibronectin type III repeat homology <FN3F>
Fi201-1078/Domain: fibronectin type III repeat homology <FN3G>
Fi201-1078/Domain: intracellular #status predicted <IPM5>
Fi251-1274/Domain: intracellular #status predicted <IPM5>
Fi251-1274/Domain: protein-tyrosine-phosphatase homology <FP12>
Fi265-1897/Domain: protein-tyrosine-phosphatase homology <PTP1>
Fi265-1897/Domain: protein-tyrosine-phosphatase homology <PTP1>
Fi265-1897/Domain: protein-tyrosine-phosphatase homology <PTP2>
Fi465-1871/Domain: protein-tyrosine-phosphate (Arg) #status predicted
Fi155-188/Active site: Cys (phosphocysteine intermediate) #status predicted
Fi1829/Active site: Cys (phosphocysteine intermediate) #status predicted
Fi1829/Active site: Cys (phosphocysteine intermediate) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 RSVSFVYYQQTLQGDFKNRAEMIDFN-----IRIKNV-TRSDAGKYRCEVSAPSEQGQN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LEEDTVTLEVLVAPAVPSCE-----VPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F.1-16/Domain: signal sequence #status predicted <SIG>
F.17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>
F.17-1250/Domain: extracellular #status predicted <EXT>
       C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C;Accession: S03841; JL0051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein K09C8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23007; T23543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKT---PKKTVXSRLEWKKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Gaps
                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-1897 <STR>
A;Cross-references: EMBL:Y00815; NID:g34266; PIDN:CAA68754.1; PID:g34267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 LLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYR 223
                                                                                                ;Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, Exp. Med. 168, 1523-1530, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.3%; Score 156; DB 1; Length 1897; Best Local Similarity 25.8%; Pred. No. 0.00039; Matches 59; Conservative 35; Mismatches 89; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37-99/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:PTPRF; LAR
A.Crояя-references: GDB:120138; ОМІМ:179590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kershaw, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ErbB Kinase activator alphal, brain and thymus - rat C;Species Rattus norvegicus (Norway rat)
C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
C;Accession: JC5701; PC4411
R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag A;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag A;Title: A novel brain-derived member of the epidermal growth factor family that interact A;Reference number: JC5700; MUID: 98006324; PMID: 9348101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                66 LGRSVSFVYYQQTLQGD--FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEE 123
                                                                                                                                                                                                                                                                                                                                                                                         DIVILEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 QSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNI----S 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 LERNQRYIFFLEPTEQPLVFKTAFAPVDPN--GKNI-KKEVGKILCTDCATRPKLKKMKS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;422-444/Domain: hydrophobic #status predicted <HYD>
F;163,294,467/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 QTGEV----SEKOSLKCEAAAGNPQPSYRWFKDGKELNR----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 QTGEV-----SEKQSLKCEAAAGNPQPSYRWFKDGKELNR----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LGRSVSFVYYQQTLQGD--FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 DTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                     36;
                                                                                                       10.3%; Score 157; DB 2; Length 860;
.larity 27.7%; Pred. No. 0.00012;
Conservative 24; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Score 157; DB 2; Length 868; 27.7%; Pred. No. 0.00013; Live 24; Mismatches 86; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukocyte antigen-related protein precursor - human N;Alternate names: leukocyte common antigen homolog N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHARKCNETAKSYCVNG-GVCY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIIAAVVVVALVISVCGLGVCY 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHARKCNETAKSYCVNG-GVCY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 GIIAAVVVVALVISVCGLGVCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Conservative
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Matches 56; Conserva
                                                                                                                                            Local Similarity
hes 56; Conserv
                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                               Query Match
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                                                                                                                                            Best Loca
Matches
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A;Cross-references: DDBJ:AB008163; NID:g3116228; PIDN:BAA25932.1; PID:g3116229
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through b C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm F;413-475/Domain: immunoglobulin homology < 1000 process p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: DDBJ:AB005060; NID:g2626738; PIDN:BAA23417.1; PID:g2626739
A.Experimental source: SK-NSH cell
C.Comment. This protein is a member of the epidermal growth factor family. It is functi
ating the differentiation of MDA-MB-453 cells.
C.Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; immun
C.Keywords glycoprotein
F.258-311/Domain: Ig-like #status predicted <IGL>
F.345-381/Domain: EGF homology <EGF>
F.346-381/Domain: EGF homology kege>
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A;Title: A novel brain-derived member of the epidermal growth factor family that intera A;Reference number: JC5700; MUID:98006324; PMID:9348101
A;Accession: JC5700
A;Accession: JC5700
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-850 <HIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAIternate names: N-CAM 2
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Accession: J8010
C;Acc
                   2715 -----LINSVDKKHFGEYLCTIRNQNGEELANAMILSEGEC-RKHPRIDIVFVCNSFI 2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 AEMIDFNIRIKAVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSAL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 SGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ErbB kinase activator alpha, brain and thymus - human
C;Species: Homo sapiens (man)
C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 FSAPKDQQV--VTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.2%; Score 155; DB 2; Length 725; 26.6%; Pred. No. 0.00015; ive 37; Mismatches 99; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neural cell adhesion molecule 2 - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 LDTGEYSCEARNSVGYRRCPGKRMQVD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.6%
Matches 55; Conservative
                                                                                                                                                                                                                        11 |:||:
2768 FSVVHVLLISI 2778
                                                                                                                                                             243 AVVVVALVISV 253
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                                                                         A,Accession: T23007
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Bolecule type: DNA
A,Cross-references: EMBL:Z68005; PIDN:CAA91994.1; GSPDB:GN00028; CESP:K09CB.5
A,Experimental source: clone F59F3
A,Experimental source: clone F59F3
B,Keference number: Z19755
A,Accession: T23543
A,Accession: T23543
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-1326 -4M12.
A,Molecule type: DNA
A,Residues: 1-1326 -4M12.
A,Cross-references: EMBL:Z68006; PIDN:CAA91999.1; GSPDB:GN00028; CESP:K09CB.5
A,Experimental source: clone K09C8
C,Genetics:
A,Gene: CESP:K09C8.5
A,Map position: X
A,Introns: 34/1; 85/3; 133/3; 182/2; 220/3; 262/2; 390/3; 442/2; 493/3; 563/2; 586/3; 61
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A;Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 252
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Argonal 13
Argonal 13
Argonal 13
Argonal 13
Argonal 14.0
Argonal 15
Accession and Argonal Elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C; Accession: T34416
B; Wohldmann, P.
Bruton, B.; Wohldmann, P.
Bruton, B.; Wohldmann, P.
Briton, E.; Wohldmann, P.
Bruton, B.; Wohldmann, P.
Briton: The sequence of C. elegans cosmid F12F3.
A; Reference number: Z21521
A; Reference number: Z21521
A; Residues: Drellminary; translated from GB/EMBL/DDBJ
A; Residues: 1-2783 <FUL>
A; Residues: 1-2783 <FUL>
A; Residues: 1-2783 <FUL>
A; Residues: 1-2783 <FUL>
A; Cross-references: EMBL: U80022; PIDN: AAC25886.1; GSPDB: GN00023; CESP: F12F3.2
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 10.2%; Score 155.5; DB 2; Length 1328; Local Similarity 27.5%; Pred. No. 0.00028; No. 42; Conservative 34; Mismatches 66; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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                                            A;Reference number: 219651
A;Accession: T23007
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 SYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVG 221
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Best Local S:
Matches 42
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Search completed: December 9, 2003, 17:13:41 Job time: 17.0557 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 9, 2003, 17:08:11; Search time 9.86411 Seconds

(without alignments)

1420.702 Million cell updates/sec
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1420.702 Million cell updates,
Title: US-09-852-797-76
Perfect score: 1521
Sequence: 1 MARRSRHELLLLRYLVVA......SSKATTMSENDFKHTKSFII 298

Sequence: 1 MARRSRHRLLLLLLRYLVVA.. Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		P57087 homo sapien	homo	m B m	pog	homod	homo	drosc	P97792 mus misculu	_	P40199 homo sapien		O35136 mus musculu	ratt	P56974 mus musculu	P10586 homo sapien	homo	O14511 homo sapien	-	008775 rattue norv		6			homo	homo	homo	1 homo	gallu	P15364 drosophila	drosophil			-
SUMMARIES	ΙD	JAM2 HUMAN	JAM1 HUMAN	JAM1 MOUSE	JAM1-BOVIN	A33 HUMAN	CXAR HUMAN	FAS2_DROME	CXAR_MOUSE			VGR2_MOUSE			NRG2_MOUSE	PTPF_HUMAN	NCM2_HUMAN	NRG2_HUMAN	1 CEA1_MOUSE	VGR2_RAT	NCA2_XENLA	ECTO_RAT	NCA1_XENLA	NCA1_CHICK	PTPD HUMAN	CEA1 HUMAN	NCA2 HUMAN	NCA1 HUMAN		AMAL_DROME	ICCR_DROME	NRG DROME	CEA8 HUMAN	NCA1_RAT
	Length DB	298 1	299 1	300 1	298 1	319 1	365 1	873 1	365 1	6632 1	344 1	1367 1	837 1	868 1	756 1		837 1			1343 1				1091 1	1912 1	526 1	761 1	848 1	1051 1	333 1	764 1	1302 1	349 1	D.
de	Query Match	99.8	28.2	27.7		15.2	12.9	12.2	11.8				٠	•	10.3		10.2	10.2	10.1	٠	•		٠	٠		7.6	٠	•	•	9.5	9.5	•	9.5	9.4
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Q14002 homo sapien	Q62718 rattus norv P20273 homo sapien	Q24372 drosophila	P31836 bos taurus	P11799 gallus gall	P98160 homo sapien	P13594 mus musculu	Pl3595 mus musculu	Q05793 mus musculu	P06731 homo sapien	Q9bzz2 homo sapien
CEA7_HUMAN	NTRI RAT CD22 HUMAN	LACH_DROME	NCA1 BOVIN	KMLS_CHICK	PGBM HUMAN	NCA2 MOUSE	NCA1 MOUSE	PGBM_MOUSE	CEAS HUMAN	SN_HUMAN
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265	344	359	853	1906	4391	725	1115	3707	702	1709
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142.5	140.5	140	140	140	140	139	139	139	138.5	138.5
3.4	3 6	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING SECONDARY LYMPHOLD ORGANS.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
                                                                                                                  SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 1 immunoglobulin-like C2-type domain. DATABASE: NAME-EVGW; NOTE-PROW 2:1-3(2001); WWW-ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              JUNCTIONAL ADHESION MOLECULE EXTRACELLULAR (POTENTIAL).
                                                                                                    SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                 ; 606870; -.
GO:0005887; C:integral to plasma membrane; NAS.
GO:0016337; P:cell-cell adhesion; NAS.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                     EMBL; AY016009; AAG49022.1; -. EMBL; BC017779; AAH17779.1; -.
                                                                                                                                                                                                                                                                                                           EMBL; AF255910; AAF81223.1; -.
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InterPro, IPR003598; Ig.c2.
InterPro, IPR003006; Ig_MHC.
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298 AA;
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C -1-FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PARD3. The association of the PARO5-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.

C -1-SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this interaction (By similarity).

C -1-SUBCELLULAR LOCATION: Type I membrane protein (Potential).

C -1-TISSUE SPECIFICITY: Localized at tight junctions of both epithelial and endothelial cells.

C -1-SIMILARITY: BELONGS TO THE IMMONOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adheeion molecule in human endochelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Naik W.P., Naik M.U., DeLeon P., Spychala J.;
"Cloning and characterization of PAM-1, a novel platelet adhesion molecule involved in platelet activation.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion molecule 1) (PAM-1) (platelet F11 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D., Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99323940; PubMed=10395639;
Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
Iwamatsu A., Kita T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and sequencing of the cDNA of F11 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel Ig superfamily member from human platelets.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                            299 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21154917; PubMed=11230166;
                                                                                                                  (Rel. 40, Created)
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                                            STANDARD;
                                                                                                                                                                                                                                                                                            OR JAMI OR JCAM.
                                                                                                                                                                                                                                                                                                                             (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                  16-0CT-2001
                                                                                                                                            16-OCT-2001
15-SEP-2003
                                        JAM1 HUMAN
Q9Y624;
JAMI HUMAN

AC D JAMI H

AC D JAMI H

AC D JAMI H

AC D JAMI H

AC D J 16-OCTA

BE JUNCTIA D

OC MAMMAN

RA D JUNCTIA D

OC BURATY

OC D JUNCTIA

RA JUMAN

RA JUMAN
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 TVXSRLEWK-KLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 DLNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKA----TTMSEN 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98327120; PubMed=9660867;
Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR0031006; Ig-MC.
InterPro; IPR003506; Ig-MC.
InterPro; IPR003506; Ig-MC.
InterPro; IPR003506; Ig-MC.
InterPro; IPR003506; Ig-M.
PR051TE; PS50835; IG-LIKE; 2.
Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane; SignAL 1 25 POTENTIAL.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
D95DE2FEA23D2851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 429; DB 1; Length 299;
Pred. No. 5.4e-29;
50; Mismatches 126; Indels
                                                                                                                                                                                                                                                                        JUNCTIONAL ADHESION MOLECULE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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15-SEP-2003 (Rel. 42, Last annotation update)
Junctional adhesion molecule 1 precursor (JAM).
                                                                                                                                                                                                                                                                                                                                          IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
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                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
EMBL; AF207907; AAF22829.1; -. EMBL; AF172398; AAD48877.1; -. EMBL; AL136649; CAB66584.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%;
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les 106, Conservative
                                              PIR; A59406; S56749.
Genew; HGNC:14685; F11R.
MIM; 605721; -.
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290 EFKQTSSFLV 299
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Mostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
Minkler F.K., Hennig M.,
Minkler F.K.,
Minkler M.,
Minkle
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Fruscella P., Panzeri C., Stoppacciaro A., AUCU D., C., Simmons D., Dejana E., "Junctional adhesion molecule, a novel member of the immunoglobulin superfamily that distributes at intercellular junctions and modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interaction.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
Localized at tight junctions of both epithelial and endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tight junction, Immunoglobulin domain, Glycoprotein, Transmembrane, Repeat, Signal, 3D-structure.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                Ebnet K., Suzuki A., Horikoshi Y., Hirose T., Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.; "The cell polarity protein ASIP/PAR-3 directly associates with junctional adhesion molecule (JAM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epithelial and endothelial cells.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JUNCTIONAL ADHESION MOLECULE 1. EXTRACELULAR (POTENTIAL).
POTENTIAL. CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
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                                                                                                                                                                                                                                    Cell Biol. 142:117-127(1998).
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MGD; MGI:1321398; F11r.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig V.
Pfam; PP00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG LIKE; 2.
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32368
                                                                                                                                                                                                                                                                                                                               INTERACTION WITH PARD3.
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185
300 AA;
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

MEDLINE=99323940; PubMed=10395639;

A Dazki H., Ishli K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,

RA Darkin H., Ishli K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,

RA Durational Adhesion molecule in human endothelial cells.",

RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution

RT "Innctional adhesion molecule in human endothelial cells.",

RL J. Immunol. 163:553-557(1999).

CC -I- FUNCTION: Seems to plays a role in epithelial tight junction

CC formation. Appears early in primordial forms of cell junctions and

recruits PARD3. The association of the PARD5-PARD3 complex may

prevent the interaction of PARD3 with JAM1, thereby preventing

CC right junction assembly (By similarity). Plays a role in

regulating monocyte transmigration involved in integrity of

epithelial barrier. Involved in platelet activation.

CC SUBUNIT: Interacts with the first PDZ domain of PARD3. The

association between PARD3 and PARD6B probably disrupts this

interaction (By similarity).

CC -- SUBCELLUIGAR LOCATION: Type I membrane protein (Potential).

CC -- TISSUE SPECIFICITY: Localized at tight junctions of both

epithelial and endothelial cells.

CC -- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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                                                                                                                                                                      64 KKL-GRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLE 122
                                                                                                                                                                                                   TRAFMNSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGI 239
                                                                                                                                                                                                                                                           EDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLG 182
                                                                                                                                                                                                                                                                                                                                              SQS-TNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVG-YRRCPGKRMQVDDLNISGI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IAAVVVVALVISVCGLGVCYAQRKGYF---SKETSFQKSNSSSKATTMSENDFKHTKSFI 297
                                                                                                             RAGRKLEFFFWILGSLVQGKGSVYTAQSDVQVPE----NESIKLTCTYSGFSSPRVEW 61
                                                                                     4 RSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEW
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea;
Bovidae, Bovinae, Bos.
                                            12;
27.7%; Score 421; DB 1; Length 300
34.6%; Pred. No. 2.6e-28;
ive 55; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Junctional adhesion molecule 1 precursor (JAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AA.
                                          104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                        Similarity
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Query Match
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117 TYGEVTVQLIVLVPPSKPTINVPSSVTIGTRAVLTCSERDGSPPSEYKWFKDGVEMPLEP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LEWK-KLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 NLEEDTYTLEVLVAPPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 NISGIIAAVVVALVISVCGLGVCYAQRKGYF--SKETSFQKSNSSSKATTMSENDFKHT 293
                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                                                                                                                                                                                                         9 LLL---LLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILAC----KTPKKTVXSR
                                                                                                                                                                                                                                                                                                                                                                                                     12 LILFTSMILCSLALGRGAVQTY-----EPVVRVPENNPAKLSCSYSGFSSP----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 RLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGK----RMQVDDL
                                                                                                                                                                                                                                                                                                                                               33; Gaps
             EMBL; AF111714; AAD42051.1; -.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Colon carcinoma;
MEDLINE=97165045; PubMed=9012807;
MEDLINE=97165045; PubMed=9012807;
Moritz R.L., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
Burgess A.W.;
                                                                                                                                                                                                                                                             POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
714FEIC1714769A2 CRC64;
                                                                                                                                                                                                                                                                                                                 27.3%; Score 415.5; DB 1; Length 298; 35.1%; Pred. No. 7.4e-28; tive 47; Mismatches 118; Indels 33.
                                                                                                                                                             JUNCTIONAL ADHESION MOLECULE EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cell surface A33 antigen precursor (Glycoprotein A33).
                                                                                                                                                                                                                      IG-LIKE V-TYPE:1.
IG-LIKE V-TYPE 2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                          32456 MW;
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 35.1%
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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2337
2337
258
258
1124
108
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298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 SSFLV 298
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Q99795;
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DOMAIN
TRANSMEM
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                     Query Match
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198 LKNISTDT-----SGYYICTSSNEEGTQFCNITVAVRSPSMVALYVGIAVGVVA 247
                                                                    191 TMNTKTGTLQFNTVSKLDTGEYSCEARNSVGWRRCP-GKRMQVDDLNIS-----GIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-22388257; PubMed=12477932; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Struler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97250541; PubMed=9096397;
Tomko R.P., Xu R., Philipson L.;
"HCAR and MCAR: the human and mouse cellular receptors for subgroup adenoviruses and group B coxsackieviruses ";
Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M., Sollerbrant K., Sonnhammer B., Philipson L.; "Putative regulatory domains in the human and mouse CAR genes."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                          (Coxsackievirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic organization and chromosomal localization of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=97190109; PubMed=9036860;
MEDLINE=97190109; PubMed=9036860;
MEDGEJSON J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg
"Isolation of a common receptor for Coxsackie B viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
Sequence and expression of CXADR, the human gene for the
coxeackievirus and adenovirus receptor.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Coxeacklevirus and adenovirus receptor precursor (C adenovirus receptor) (HCAR) (CVB3 binding protein).
                                                                                                                                                                                                                                                                                                     CXAR HUMAN STANDARD, PRT; 365 AA. P78310; 000694; 30-MX-2000 (Rel. 39, Created) 30-MX-2000 (Rel. 39, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20008750; PubMed=10543405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coxsackievirus B-adenovirus rec
Hum. Genet. 105:354-359(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 275:1320-1323(1997).
                                                                                                                                                                               243 AVVVVALVISVC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adenoviruses 2 and 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CXADR OR CAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowles N.E.
                                                                                                                                                                                                                                                                                   CXAR_HUMAN
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                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 LVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPKDOQVVTAVXYQEAILACKTPKKTVXSR---LEWKKL----GRSVSFVYYQQT-LQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVETPODVLRASOGKSVTLPC-TYHTSTSSREGLIOWDKLLLTHTERVVIWPFSNKNYIH 81
                                                                                                                                                                                                                 Gaps
  human A33 antigen is a transmembrane glycoprotein and a novel
                                                                                                                                                                                          "Characterization of posttranslational modifications of human A33
                                                                                                                                                                                                                                                                                                                                                                   PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to plasma membrane; TAS
                                                                                  POST-TRANSLATIONAL MODIFICATIONS.
MEDLINES-97386159; Pubmed-9245713;
Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
9BFC7AAF45C2408E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 2. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 2. Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein; Transmembrane; Signal; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 231; DB 1; Length 319
28.6%; Pred. No. 2.9e-12;
w.omatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL SURFACE A33 ANTIGEN. EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
                      member of the immunoglobulin superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U79725; AAC50957.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                PTM: PALMITOYLATED.
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319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
72; Conserv
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236
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146
162
                                                                                                                                                                          Simpson R.J.
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TRANSMEM
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DISULFID
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A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A., A Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blackesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length I.T. human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-! FUNCTION: SERVERS AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).

-! SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004872; F:receptor activity; TAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig c2.
InterPro; IPR003006; Ig_MHC.
FF4m; PF000407; Ig; 2.
FRANKT; SM0408; IGc2; 1.
PROSITE; PSS0835; IG_LIKE; 2.
Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB01C6346CB7FE64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF169366; AAF05908.1;
AF169366; AAF05908.1;
AF169366; AAF05908.1;
AF169361; AAF05908.1;
AF169362; AAF05908.1;
AF169363; AAF05908.1;
AF169363; AAF05908.1;
AF169365; AAF05908.1;
AF169365; AAF05908.1;
AF169365; AAF05908.1;
AF169365; AAF01088.1;
AF242865; AAF01088.1;
AF242864; AAG01088.1;
AF242864; AAG1088.1;
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PDB; 1FSW; 08-NOV-00.
PDB; 1KAC; 24-NOV-99.
Genew; HGNC:2559; CXADR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; 3D-structure
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TRANSMEM
DOMAIN
DOMAIN
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EMBL;
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61 PADNQKVDQ-VIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQ 119
                                                                                                                                                                                                                          REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENTINE-Berkeley;

RA

Redame M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA

Ramatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA

Recorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA

Randon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Freiffer B.D.,

RA

Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA

Ballew R.M., Basu A., Baxendal J., Bayraktaroglu L., Beasley E.M.,

RA

Ballew R.M., Basu A., Barendal J., Bayraktaroglu L., Beasley E.M.,

RA

Ballew R.M., Basu A., Barendal J., Bayraktaroglu L., Basley E.M.,

RA

Bartis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA

Rockova D., Botchan M.R., Bouck J., Brokstein P., Brotister P.,

RA

Roberty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA

Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Pleischmann W.,

RA

ROGSON K., Doup L.E., Downes M., Dugan-Rocha S., Plunkov B.C., Dunn P.,

RA

ROGSON K., Gabrelian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA

Roldek A., Gong F., Gorrell J.H., Re Z., Kenrison J.A., Recchum K.A.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Ibegwam C.,

Aulali M., Kalush F., Karpen G.H., Ke Z., Kenrison J.,

Ranktei B., McInteon T.C., McLeod M.P., Moshrefi A.,

Aulali M., Maltei B., McIntesh T.C., McLeod M.P., Moshrefi A.,

Robon K., Nelson D.R., Nark, Naurphy L., Marny D.M., Nalson D.L.,

RA

Mount S.M., Moy M., Murphy B., Murphy L., Marny D.M., Nalson D.L.,

Rad Roberts D. R., Rad R., Marny D. R., Nalson D.R., Rad R., Rad R., Rad R., Rad R., Rad
                                                                                                                                                                                                                                                                                             169 FKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGK 228
                                                                                                                                                                                                                                                                                                                                               176 QK------LSDSQKMPTSWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLLR 226
64 ----KKLGRSVSFVYYQQTLQGDF-----KNRAEMIDFNIRIKNVTRSDAGKYR
                                                                                                                                                                                        109 CEVSAPSEQGONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grenningloh G., Rehm B.J., Goodman C.S.;
"Genetic analysis of growth cone guidance in Drosophila: fasciclin II
functions as a neuronal recognition molecule.";
Cell 67:45-57(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P340B2; P340B3; Q94M46;

01-FBB-1994 (Rel. 28, Created)

01-FBB-1994 (Rel. 28, Last sequence update)

15-SEP-2003 (Rel. 22, Last amnotation update)

FASC OR EG:EG0007.3 OR CG3665.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                       229 RMQVDDLNISGIIA-AVVVVALVISVCGLGVCYAQRKGYFSKETSFQK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                      227 INVVPPSNKAGLIAGAIIGTLIALALALIGLIFCCRKK---RREEKYEK 271
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12.9%; Score 195.5; DB 1; Length 365; 23.3%; Pred. No. 3.4e-09; ive 57; Mismatches 123; Indels 41;

67; Conservative

Matches

Similarity

Query Match Best Local

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Query Match
Best Local Similarity
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CARBOHYD
VARSPLIC
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang S., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wangsaarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Zheng R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=3; Synonyms=B;
Isold=P34082-3; Sequence=VSP_002506, VSP_002507;
IISSUE SPECIFICITY: In embryos, both isoforms are initially
expressed on the surface of the axons in the MPI pathway and later
on several other longitudinal axon fascicles.
SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Oregon_R,
MEDLINE=20196011; PubMed=10731137;
MEDLINE=20196011; PubMed=10731137;
MEDLINE=20196011; PubMed=10731137;
MEDLINE=20196011; PubMed=10731137;
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D., Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Campbell L.A., Darlamitsou A., Henderson N.S., Momillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., Groy A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Neuronal recognition molecule for the MP1 axon pathway, pathway recognition for axons during the development of nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLILAR LOCATION: Type I membrane protein (isoform 1); attached to the membrane by a GPI-anchor (isoform 2).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "From sequence to chromosome: the tip of the X chromosome of D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1; Synonyms=A, Membrane-linked;
IsoId=P34082-1; Sequence=D1splayed;
Name=2; Synonyms=C, Phospharidylinositol-linked;
IsoId=P34082-2; Sequence=VSP_002508, VSP_002509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                          [3]
REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                       STRAIN=Berkeley; MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster.";
Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 22-873 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systematic review.";
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Lewis

EMBL; M77165; AAA28527.1; -.

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83
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ANNNLGTLLYSAGFNSGVGALHKRLFTTTTTTATSTTTIT
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1. Similarity 24.6%; Pred. No. 6.1e-08;
67; Conservative 50; Mismatches 101; Indels 54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIDVIQVAERQVFSSAAIVGIAIGGVLLLLFVVDLLC
DNPHPSTSGAAPLAQLLVIFTALPTMLLILPPTTHTA
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                                                                                                                                                                                          R GO; GO:0005916; P:bomophilic cell adhesion; IDA.

R GO; GO:0007156; P:homophilic cell adhesion; IDA.

GO; GO:000711; P:learning and/or memory; IMP.

R GO; GO:0008038; P:mushroom body development; IMP.

R GO; GO:0008038; P:mushroom body development; IMP.

R GO; GO:00045473; P:response to ethanol (sensu Insecta); NAS.

R InterPro; IPR003501; FN III.

R InterPro; IPR003506; Ig_C2.

R InterPro; IPR00306; Ig_MHC.

R Pfam; PF00041; fn3; 2.

R Pfam; PF00047; ig; 5.

R SMART; SM0060; FN3; 2.

R SMART; SM0060; FN3; 2.

R R RAT; SM00408; IGC2; 3.

R PROSITE; PS50835; IG LIKE; 5.

Cell adhesion; Glycoprotein; Repeat; Alternative splicing;

M Immunoglobulin domain; Transmembrane; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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/FTIda-VSP 002569.
S -> R (IN REF. 4; CAA21826).
E48F0484CCE62AC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FASCICLIN II.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC
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EMBL; AL033125; CAA21825.1; --
EMBL; AE003430; AAF45925.2; --
EMBL; AE003430; AAN09119.1; --
EMBL; AL033125; CAA21826.1; --
PIR; A41054; A41054.
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                   KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 143
                                                                                                                   VSKLDTGEYSCEARNSVGYRRCPGK----RMQVDDL-NISGIIAAVVVVALVISVCGLG 257
                                                                           240 BAVEGKPFAANCTAR-GKPVPEISWIRDATQL-----NVATADRFQVNPGTGLVTISS
                                                           SALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomko R.P., Xu R., Philipson L.; and Mouse cellular receptors for subgroup C adenoviruses and MoAR: the human and mouse cellular receptors for subgroup C proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=97190109; PubMed=9036860;
BEDGELSON J.M., Cunningham J.A., Droguett G., Kurt.-Jones B.,
Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
"Isolation of a common receptor for Coxsackie B viruses and
adenoviruses 2 and 5.";
                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                   CXAR_MOUSE STANDARD; PRT; 365 AA.
P97792; 009052;
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Liver;
Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
The wurine CAR homologue (mCAR) is a receptor for coxsackie B viruses and adenoviruses.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLUJAR LOCATION: Type I membrane protein.
--- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                258 VCYAQRKGYFSKETSFQKSNSSSKATTMSEND 289
                                                                                                                                                                                                    | | | | : : | : : | TCRA--KGRPAPAITFRRWGTQEEYTNGQQDD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C3H/MAI;
MEDLINE=97250541; PubMed=9096397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1201679; Cxadr.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . . .) (POTENTIAL).

N-AAPNILSRMGAVPUMIPAQSKDGSIV -> FKYAXKTDGIT
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                                                                                                                                                                                                                                                                                                                                                                28 GFSAPKDQQVVTAVXYQEAILACK---TPKKTVXSRLEW-----KKLGRSVSFVY----
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            PROSITE; PSS0835; IG_LIKE; 2.
Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                   Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=96180278; PubMed=8603916;
Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
"The Caenorhabditis elegans gene unc-89, required for muscle M-line assembly, encodes a giant modular protein composed of Ig and signal transduction domains ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           001761, Q17362,
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Muscle M.line assembly protein unc-89 (Uncoordinated protein 89)
                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                       Length 365;
                                                                                                                                                                                                                                                                                                     ; Score 180; DB 1; Length 365; Pred. No. 6.8e-08; 44; Mismatches 130; Indels
                                                                                                       EXTRACELLULAR (POTENTIAL).
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5445B4B52A34B2A2 CRC64;
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23.7%;
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SMART; SM00408; IGC2; 1.
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CRC64;
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IG-LIKE C2-TYPE 10.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 12.

IG-LIKE C2-TYPE 14.

IG-LIKE C2-TYPE 16.

IG-LIKE C2-TYPE 16.

IG-LIKE C2-TYPE 19.

IG-LIKE C2-TYPE 19.

IG-LIKE C2-TYPE 21.

IG-LIKE C2-TYPE 31.

IG-LIKE C2-TYPE 41.

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The SWISS-PROY entry is one property in the produced through a collaboration between the Swiss Proy entry is copyright. It is produced through a collaboration between the Swiss Proy entry is copyright. It is produced through a collaboration between the Swiss Proy entry is copyright. It is produced through a collaboration between Bointchart of Education and Itela Entry and Itela Swisseness as long as its content is in no way can differ require a license spread to the Swisseness and itelas a content is in no way can differ require a license spread to the Swisseness and Itelas Swisseness as long as its content is in no way can differ require a license spread to the Swisseness and Itelas Swisseness as long as its content is in no way can differ the Swisseness and Itelas Swisseness as license spread to the Swisseness and Itelas Swis
                                                                                                                   Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

-!-PUNCTION: Structural component of the muscle M-line. Myofilament lattice assembly begins with positional cues laid down in the basement membrane and muscle cell membrane. UNC-89 responds to these signals, localizes, and then participates in assembling an M-line.

--- TISSUE SPECIFICITY: Localizes to the middle of A-bands.

--- SIMILARITY: Contains 1 DBL-homology (DH) domain.

--- SIMILARITY: Contains 1 pH domain.

--- SIMILARITY: Contains 1 PH domain.

--- SIMILARITY: Contains 1 PH domain.

--- SIMILARITY: Contains 1 SH3 domains.
STRAIN=Bristol N2;
Du Z., Le T.T., Wilson R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                          [3]
REVISIONS.
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GPI-anchor.

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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
Muman and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. 10.8.0.8.16899-16903(2002).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchc.-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CEA
                                                                                                  SUBFAMILY.
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                                                                                                 3862
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                                                                                                                                                                                           P------SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST 186
                                                                                                                              NRAEMID----FNIRIKAVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blate N. K.,
A plachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blate N. K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Holsesley R.W., Tuckhman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                               GFSAPKDQQVV---TAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFK 84
                                                                                     3813 GRGAPEFVELLRSCTVTEKQQAILKCKV-KGEPRPKIKWTKEGKEVEM-----SAR
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                       CEA6_HUMAN STANDARD; PRT; 344 AA.
P40199; Q14920;
01-FEB-1995 (Rel. 31, Created)
15-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Carcinoembryonic antigen-related cell adhesion molecule 6 precursor (Normal cross-reacting antigen) (Nonspecific crossreacting antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89122014; PubMed=3220478; Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.; Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.; Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and CEA and suggestion of nonrandom sequence variation in their conserved loop-domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tawaragi Y., Olkawa S., Matsucka Y., Kosaki G., Nakazato H., "Primary structure of nonspecific crossreacting antigen (NCA), a member of carcinoembryonic antigen (CEA) gene family, deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                  52;
 Length 6632;
                                  Indels
                                                                                                                                                                                                                                                                                  3970 -----NLDDGTQRLTVTNAKLDDMDEYRCEASNEFG 4000
                                                                                                                                                                                                                                                            187 NSSYTMNTKTGTLQFN-TVSKL-DTGEYSCEARNSVG 221
                              75;
11.2%; Score 171; DB 1; 28.1%; Pred. No. 1.3e-05; ive 29; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ochem. Biophys. Res. Commun. 150:89-96(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Lung carcinoma;
MEDLINE=88106638; PubMed=3337731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932;
                                61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3enomics 3:59-66(1988)
                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CD66c antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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Query Match
Best Local S:
Matches 61
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 TVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD 208
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REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
FORDABLE.
FROBABLE.
FROBABLE.
N-LINKED (GLCNAC. .) (POTENTIAL).
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CARCINOEMBRYONIC ANTIGEN-RELATED CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSS0815; IG_LIKE; 2.
Immunoglobulin domain; Antigen; Signal; Glycoprotein; GPI-anchor;
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD66c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd66c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Indels
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39 V -> G (IN REF. 1).
37237 MW; 4322C5D6E25849F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 163980; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR00110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 164; DB 1;
Pred. No. 1.4e-06;
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                                                                                                                                                                                                                                                                                                                                       EMBL; M18728; AAA59907.1; -.
EMBL; BC005008; AAH05008.1; -.
Genew; HGNC:1818; CEACAM6.
MIM; 163980; -.
                                                                                                                                                                                                                                                                                                                     EMBL; M29541; AAA59915.1; -.
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SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-

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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
(VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDINE-914123989; MEDINE-9114125; PubMed-8423988; Oclirichs R.B., Reid H.H., Bernard O., Ziemiecki A., Wilks A.F.; Oclirichs R.B., a putative receptor protein tyrosine kinase isolated from "NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from EIO embryonic neuroepithelium is expressed in endothelial cells of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93361481; PubMed-8356051;
Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;
Quinn T.P., Rinase I is a receptor for vascular endothelial growth factor and is selectively expressed in vascular endothelium.";
Proc. Natl. Acad. Sci. U.S.A. 90:7533-7537(1993)
-! FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF VASCULAR PERMINABILITY.
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SUBCELULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT HEART, LUNG, KIDNEY, BRAIN AND SKELETAL MUSCIE, BUT IS ALSO EXPRESSED AT LOWER LEVELS IN MOST OTHER ADULT TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A receptor tyrosine kinase cDNA isolated from a population of enriched primitive hematopoietic cells and exhibiting close genetic linkage to c-kit.";
Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c; TISSUE=Embryo;

MIDLINES-93208880; PubMed=7681362;

Millauer B., Wizigmann-Voos S., Schnurch H., Martinez R.,

Mueller N.P.H., Risau W., Ullrich A.;

"High affinity VEGF binding and developmental expression suggest

FIR-1 as a major regulator of vasculogenesis and angiogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96032749; PubMed=7559454;
Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.
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                                                                       337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C3H/He; TISSUE=Fetal liver; MEDLINE=2202084; PubMed=1717995; Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G. Lentshcka I.R.;
                                       SGSYMCQAHNS----ATGLMRTTVTMITVSGSAPVLSAVATVGITIGV
TGEYSCEARNSVGYRRCPG-KRMQVDDLNISG---IIAAVVVVALVISV
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SEQUENCE OF 1-15 FROM N.A.
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Oncogene 8:11-18(1993).
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P35918;
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ID VGR2_MOUSE

ID VGR2_MC

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DE (VEGFR)

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                                                                                                                                                                                                                                                                                    Prodom, PD000001; Prot. kinase; 2.
SMART; SM00408; 1GC2; 1.
SMART; SM00219; TyrKc; 1.
SMART; SM00219; TyrKc; 1.
SMOSITE; PS50035; IG LIKE; 5.
PROSITE; PS50010; PROTEIN KINASE DOM; 1.
PROSITE; PS50010; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ANGIGENESS, Signal; Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycolprotein; Phosphorylation; ATP-binding;
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          PROTEIN KINASES.
SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 7.
PROTEIN KINASE.
ATP (BY SIMILARITY).
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InterPro; IPR000719; Prot kinase.
InterPro; IPR001824; RTKinaseIII.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                          EMBL; X70842; CAAS0192.1; -.
EMBL; X59397; CAA42040.1; -.
EMBL; S53103; AAB25643.1; -.
EMBL; X89777; CAA61917.1; -.
PIR; A41228; A41228.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                        Ig-like.
Ig c2.
                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 6.
Pfam; PF00069; pkinase; 1
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InterPro; IPR003598;
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                                                                                                                                                                                                                                                                                                                                                                    131 LVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSY 190
                                                                                                                                                                                                                                                 622 ILIVAFQNASLQDQGDYVCSAQDKKTKKRHCLVKQLIILERMAPMITG-NLENQTTTI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCM2 MOUSE STANDARD; PRT; 837 AA.
035136, 035962;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM SHORT).
STRAIN=C57BL/6J; TISSUB=Olfactory epithelium;
MEDLINE=97476194; PubMed=9334170;
Alenius M., Bohm S.;
"Identification of a novel neural cell adhesion molecule-related gene with a potential role in selective axonal projection.";
J. Biol. Chem. 272:26083-2608(1997).
--- FUNCTION: May play important roles in selective fasciculation and
                                                                                                                                                                                                                       44 QEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFN-----
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zone-to-zone projection of the primary olfactory axons.
SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and attached to the membrane by a GPI-anchor (short isoform).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOId=035136-2; Sequence=VSP 002590;
TISSUE SPECIFICITY: EXPRESSED IN SUBSETS OF BOTH OLFACTORY AND
VOMERONASAL NEURONS IN A ZONE-SPECIFIC MANNER.
P -> T (IN REF. 1).
G -> D (IN REF. 3).
LV -> VL (IN REF. 1).
S -> C (IN REF. 1).
QLTSCLNGSGPVPAPPPTPGNHERGAA -> RSPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "OCAM: A new member of the neural cell adhesion molecule family related to zone-to-zone projection of olfactory and vomeronasal
                                                                                                                                                    Length 1367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
                                                                                                                                                10.6%; Score 160.5; DB 1; Length : 24.8%; Pred. No. 1.5e-05; ive 23; Mismatches 75; Indels
                                                                                          (IN REF. 3).
W: EFC99704F1DCA266 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
STRAIN=BALB/c, TISSUE=Olfactory neuroepithelium;
MEDLINE=97368238; PubMed=9221781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             TMNTKTGTLOFNTVSKLDTGEYSCEARNSVGYRR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TI------RRVRKEDGGLYTCQACNVLGCAR 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=035136-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kagamiyama H., Mori K.;
"OCAM: A new member of the neural
                                                                                                             1367 AA; 152516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurosci. 17:5830-5842(1997).
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 CONFLICT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSFVYYQQTLQGDFKNR-AEMIDFNIRIKNVTRSDAGKYRCE--VSAPSEQGQNLEEDT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 IIVIVNVPPAIMMPQKSFNATAERGEEMTLTCK-ASGSPDPTISWFRNGKLIEENEKYIL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 VTLEVLVAPPAV -- PSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLENGLGLGAIIGLGWAALLLILVYTDVSCPFIROCGLLMC
ITRRMCGKKSGSSGKSKELEEGKAAYLKDGSKEPIVEMRTE
DERITNHEDGSPVNEPNETTPLTEPEKLPLKEENGKEVLNA
ETIEIKVSNDIIGSKEDDIKA -> NCCEANKGENGGOSWH
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InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

InterPro; IPR007100; Ig-like.

InterPro; IPR007100; Ig-like.

R InterPro; IPR007100; Ig-like.

R Ffam; PR00047; Ig. 5.

R MART; SW00408; IGc2; 5.

R PR0071TE; PS0835; IG LIKE; 5.

R PR0071TE; PS0835; IG LIKE; 5.

W Cell adhesion; Transmembrane; Glycoprotein; Repeat;

Immunoglobulin domain; Signal; GPT-anchor; Alternative splicing.

T SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
            SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                              NEURAL CELL ADHESION MOLECULE EXTRACELLULAR (POTENTIAL).
BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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(GLCNAC. . . )
                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
FIBRONECTIN TYPE-111 1
FIBRONECTIN TYPE-111 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 QSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVG 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 159.5; DB ilarity 29.7%; Pred. No. 1e-05; Conservative 34; Mismatches :
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-i- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF THE PROPEDIATION OF THE PROPEDIATION OF THE PROPEDIATION OF THE PROPEDIATION (BY SIMILARITY).

-i- DOMAIN: REBE RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN: REBER RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE.

-i- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTENSAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM (BY SIMILARITY).

FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM.
NEUREGULIN-2.
EXTRACELLULAR (POTENTIAL).
INTERNAL SIGNAL SEQUENCE (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IGHLIKE C2-TYPE.
SER.THR-RICH.
EGF-LIKE.
POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00022; EGF 1: 1.
PROSITE; PS0186; EGF 2: 1.
PROSITE; PS01186; EGF 2: 1.
PROSITE; PS50835; IG LIKE; 1.
Growth factor; EGF 11ke domain; Immunoglobulin domain; Glycoprotein; Transmembrane; Multigene family; Alternative splicing.
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                                                                                                                              SIMILARITY).
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (in isoform 7).
/FTId=VSP 003465
PLV -> FFF (in isoform 3).
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PTR, JGS701; JGS701.
PTR, JGS702; JGS702.
HSSP; Q12784; JHRE.
InterPro; JRR006210; EGF_like.
InterPro; JRR007110; IGGF.
InterPro; JRR007110; IGGF.
InterPro; JRR003598; Ig_c2.
InterPro; JRR003106; Ig_MHC.
InterPro; JRR003106; Ig_MHC.
Pfam; PP00008; EGF; 1.
Pfam; PP000047; ig; 1.
Pfam; PP02158; Neuregulin; 1.
SWART; SM00168; EGF; 1.
                                                                                                                                                                                                                                                                                                        EMBL; D89995; BAA23344.1; -. EMBL; D89996; BAA23345.1; -. EMBL; D89997; BAA23346.1; -. EMBL; D89998; BAA23347.1; -.
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LGRSVSFVYYQQTLQGD--FKWRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEE 123
                                                                                                                                                                                                                                                                                                   124 DTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGS 183
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                                                                                                                                                                                                                                                                                                                                                                                           -> VGYTGDRCQQFAMV
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 47, Last amotation update)
15-SEP-2003 (Rel. 47, Last amotation update)
(Divergulin-2 precursor (Pro-NRG2) (Contains: Neuregulin-2 (NRG-2) (Divergent of neuregulin 1) (DON-1)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Choroid plexus;
MEDLINE=97342638; PubMed=9199335;
Busfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J.,
Woolf E.A., Comrack C.A., Dussault B.J., Woolf J., Goodearl A.D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6; TISSUE=Brain; MEDILNE=97311398; PubMed=9168115; Carraway K.L. III, Weber J.L., Unger M.J., Ledesma J., Yu N., Gassmann M., Lai C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Neuregulin-2, a new ligand of ErbB3/ErbB4-receptor tyrosine
                                                                                                                                                                                                                                        10.3%; Score 157; DB 1; Length 868; 27.7%; Pred. No. 1.7e-05; tive 24; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A)
                             Missing (in isoform 5).
/FTId=VSP 003468.
NGFFGQRCLEKLPLRLYMPDPKQ
         G (in isoform 5).
i=VSP_003467.
  FTId=VSP 003466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    756 AA
                      FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                        239 GIIAAVVVVALVISVCGLGVCY 260
                                                                                                                                                                                                                                                                                                                                                                                                                                              GHARKCNETAKSYCVNG-GVCY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                    868 AA; 93776 MW;
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 387:512-516(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                              117
           388
                                868
                                                      412
                                                                                      421
                                                                                                                      421
                                                                                                                                          439
                                                                                                                                                                             868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                     l Similarity
56; Conserv
                                389
                                                                                      390
                                                                                                                      414
                                                                                                                                          414
                                                                                                                                                                            440
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P56974;
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                                                                                                                                                                                              CONFLICT
CONFLICT
SEQUENCE
           VARSPLIC
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The experienciation of a neuropalin-related gene to 00-1, this highly experienced in restricted regions of the cerebalium and hippocampus"; whole cell also 11:1007-1014(1929).

1- FORTION DIRECTLIAND OF REBBB AND FERBA TREGEROMS. RESERVING THE TREAD CONTRINGUES AND ALLO PROMOTE THE AND ASSEMBLY PRESENTED WAS DESCRIBED AND THE PRESENTANCE THE AND ASSEMBLY PRESENTED WAS DESCRIBED AND ALLO PROMOTE THE AND ASSEMBLY PRESENTED WAS DESCRIBED AND ALLO PROMOTE THE AND ASSEMBLY PRESENTED WAS DESCRIBED AND ALLO PROMOTE THE AND ASSEMBLY PRESENTED WAS DESCRIBED AND ALLO PROMOTE THE AND ASSEMBLY PRESENTED WAS DESCRIBED AND ALLO PROMOTE THE AND ASSEMBLY PRESENTED WAS DESCRIBED AND ALLO PROMOTE THE AND ASSEMBLY AND ASSEMBLY PRESENTED WAS DESCRIBED AND ASSEMBLY PRESENTED AND ASSEMBLY PRESENTED WAS DESCRIBED AND ASSEMBLY PRESENTED AND ASSEMBLY AND ASSEMBLY PRESENTED AND ASSEMBLY PRESENTED AND ASSEMBLY AND ASSEMBLY PRESENTED ASSEMBLY PROPERIES AND ASSEMBLY PRESENTED AND ASSEMBLY PRESENTED ASSEMBLY PROPERED AND ASSEMBLY PROPERED AND ASSEMBLY PRESENTED ASSEMBLY PROPERED AND ASSEMB
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LGRSVSFVYYQQTLQGD--FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEE 123
                                                                                                                                                                                                                                                                                                                        183
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTIGHVSP 003462.
Missing (In 1soform DON-1S).
/FTIGHSO 003463.
VGYTGDRCQQPAMVNFSKHLGFELKE -> NGFFGQRCLEK
LPLRLYMPDFKQK (In 1soform DON-1M).
                                                  Missing (in isoform NRG2-10).
/FITd=VSP 003461.
VGTGDRGQDRAWNESKHLGFELKBAEELYQKRVLTITGI
CVALLVVG -> NGFFGGRCLEKLEFLRELXMPDPRQSYLMDT
PGTGVSSSQWSTSPSTLDLN (in isoform DON-1S).
                                                                                                                                                                                                                                                                                                                                                                                 153 QTGEV-----SEKQSLKCEAAAGNPQPSYRWFKDGKELNR----S
                                                                                                                                                                                                                                                                                                                                                                DTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGS
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.; "A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90316093; PubMed=1695146; Streuli M., Krueger N.X., Thai T., Tang M., Saito H.; Ustreuli M., Krueger N.X., Thai T., Tang M., Saito H.; Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and LAR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.; M. new member of the immunoglobulin superfamily that has a cytoplasmic region homologue to the leukocyte common antigen."; Exp. Med. 168:1523-1530(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48)
PTPRF OR LAR.
 N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                            36;
               (POTENTIAL)
                                                                                                                                                                                                                                              10.3%; Score 156; DB 1; Length 756; 27.7%; Pred. No. 1.7e-05; Live 24; Mismatches 86; Indels
                   KED (GLCNAC. . .) (POTEN
G (in isoform NRG2-10).
                                                                                                                                                                                                    /FTId=VSP_003464.
51D85DC918BE678E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989)
                                         FTId=VSP_003460
                (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1897 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIIAAVVVVALVISVCGLGVCY 260
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                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                  756 AA; 82213
                                                                                                                                                                                                                                                                           Conservative
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254
296
280
                                                      756
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                                                                                                                                                                                                                                                           Similarity
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                                                      281
                                                                                                                                            331
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            CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
 CARBOHYD
                                                      VARSPLIC
                                                                                  VARSPLIC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     MIMM; 1/920/; -. Gintegral to plasma membrane; TAS. GO; 0005887; C:integral to plasma membrane; TAS. GO; GO:0005901; F:transmembrane receptor protein tyrosine pho. . .; TAS. GO; GO:0007155; P:cell adhesion; TAS. GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . .; TAS.
                                                                                                                CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                      (FTRASE).
FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE FIRST ONE.
) J. 9:2399-2407(1990).
PUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR. IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bu (GLCNAC. ...) (POTENTIAL).
TO (GLCNAC. ...) (POTENTIAL).
GGLCNAC. ...) (POTENTIAL).
(GLCNAC. ...) (GLCNAC. ...)
                                                                                                                            tyrosine + phosphate.
-- SUBCELLUIAR LOCATION: Type I membrane protein.
-- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-- SIMILARITY: Contains 8 fibronectin type III domains.
-- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PSSO815, IG LIKE, 3.
PROSITE, PSCO815, TYR PHOSPHATASE 1; 2.
PROSITE; PSSO056; TYR PHOSPHATASE 2; 2.
PROSITE; PSSO055; TYR PHOSPHATASE PTP, 2.
Hydrolage; Receptor; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439850F1D5C031FF CRC64;
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003961; FILTIMEMBERIAL INTERPRO; JUN07189; FILTIMEMBERIAL INTERPRO; IPR003962; FITII subd.
InterPro; IPR003962; FITII subd.
InterPro; IPR003109; IQ -11 ike.
InterPro; IPR003899; IQ -2.
InterPro; IPR003897; TYR phosphatase.
InterPro; IPR00387; TYR phosphatase.
InterPro; IPR00041; IQ; 3.
Pfam; PP00041; Iq; 3.
Pfam; PP00041; iq; 3.
Pfam; PR00102; X_phosphatase; 2.
PRINTS; PR00104; PRNYPBIII.
SMART; SM00060; FN3; 4.
SMART; SM00060; FN3; 4.
SMART; SM0014; PPPC; 2.
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                                                                                                                                                                                                                                                                                                                                                             EMBL; Y00815; CAA68754.1; -. PIR; S03841; TDHULK.
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                                                                                                                                                                                                                                                                                                                                                                             PIR; S03841; TDHULK.
PDB; 1LAR; 25-APR-00.
Genew; HGNC:9670; PTPRF.
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1274
1897
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SIGNAL
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TRANSMEM
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Search completed: December 9, 2003, 17:11:45 Job time : 11.8641 secs

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9, 2003, 17:08:46 ; Search time 32.1882 Seconds (without alignments) 2389.068 Million cell updates/sec
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1 MARRSRHRLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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Bp_vertebrate:*
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
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                                                                                                                                                                                                                                                                                                     December
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ogits misculu		811	800	mus.		09d1m9 musculu	Ogbx67 homo ganien	O8wwl8 homo ganien	O96fll homo manien	OBVC39 mm Billion	09thvl rattus norw	Ogyaho pamian	Ogikas rattus nom	Ogles renous las	Q9pwr4 gallus gall
SUMMARIES	D	09J159	Q8CE95	QBC5K9	60CMD6	Q9D8B7	Q9EPK4	Q9D1M9	Q9BX67	OBWWL8	Q96FL1	O8VC39	09JHY1	O9Y5B2	09JKD5	091664	Q9PWR4
	DB	7	11	11	11	11	11	11	4	4	4	11	11	4	11	13	13
	Query Match Length DB	298	298	298	181	310	310	310	310	355	309	300	300	259	173	318	335
مهن	Query	79.9	79.7	79.7	33.4	32.8	32.8	32.6	31.6	31.6	31.6	27.7	26.9	25.9	20.7	14.9	14.8
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335 319 319 139 135	181 259 4 319 6	390 365 4 4 4	344	390 6 372 1 319 6	430 4 773 5 300 1	300 1 352 1 365 1	304 323 4 284 4	325 4 327 4 344 1 358 1
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ALIGNMENTS

RESULT 1

09J159;
DT 00J159;
DT 01-0CT-2000 (TERMBLEE] 15, Last sequence update)
DT 01-MAR-2003 (TERMBLEE] 15, Last sequence update)
DE 01-0CT-2000 (TERMBLEE] 19, Last annocation update)
DE 01-0CT-2000 (TERMBLEE] 19,

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Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Sukuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Puruno M., Aono H., Baldarchili R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Naturcional annotation of a full-length mouse cDNA collection.";
EMBL; AJ29175; GAC206991;
BEBL; AJ29175; GAC206991;
BEBL; AJ29175; GAC206991;
BEBL; AZ01914; BAB290631;
BEBL; AZ01914; BAB290631;
BEBL; AZ01914; BAB290631;
BIRCEPPC; IPR00110; 19-1ike.
BEBL; PLOS BEBL; PR00110; 19-1ike.
BEBL; PLOS BEBL; PR00110; 19-1ike.
BEBL; PLOS BEBL; PR001006; 19-MC.
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Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ol-Mar-2003 (TrEMBLrel. 23, Last annotation update)
Unortion cell adhesion molecule 2.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Musinae; Musin
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MEDINE=22354683; Pubmed=12466851;
The FANTOM CONSORTIUM;
the RIKEN Genome Exploration Resean
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PROSITE; PS50835; I
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STRAIN=C5-BL/6J; TISSUE=Medulla oblongata;
MEDLINE=223-84683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AKO78128; BAC37139.1; -.
SEQUENCE 298 AA; 33182 MW; 1131F0BFD89CEB51 CRC64;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                     5;
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EMBL; AK028757; BAC26102.1; -.
SEQUENCE 298 AA; 33079 MW; CB8227EC13D349A3 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                        37;
                                                                            DB 11;
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78.6%; Pred. No. 3.5e-104;
iive 25; Mismatches 37;
                                                                    79.7%; Score 1212; DB 11; 78.3%; Pred. No. 3.5e-104; iive 26; Mismatches 37;
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                                                                  Query Match 79.7%;
Best Local Similarity 78.3%;
Matches 234; Conservative
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Matches 235; Conservative
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120 NLEEDTVTLEVL 131
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A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Azawa K., Izawa M., Nishi K., Kyosawa H., Adachi J., Fukuda S.,

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A Azawa K., Izawa M., Nishi K., Kyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Jashun T., Golobori T., Bono H., Kasukawa T., Saito R.,

A Radota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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Baka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Wanjor L.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

By Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Namanaka J., Saraki S.,
240 IIATVVVVAFVISVCGLGTCYAQRKGYFSKETSFQKGSPASKVTTMSENDFKHTKSFII 298
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
2410167M24Rik protein (Junction cell adhesion molecule 2)
JCAM2 OR 2410167W24RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; Ig; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
SRQUENCE 181 AA; 20330 MW; 603B6114FBB11AEB CRC64;
                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J;
MEDLINE=22354683; PubMed=12466851;
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EMBL; AKO10826; BAB27208.1; -.
EMBL; AKO45095; BAC32219.1; -.
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                                                                                                                                                              PRELIMINARY;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Yamanaka I., Radacaki Y., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsudo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Radaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rordone P., Marchionni L., Machima J., Mazzarelli J., Mombaette P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hapsahizaki Y.; Radotaki S., Matuki H., Toyo-oka K., Wang K.H., Wettz C., Whittaker C., Wilming L., Matuki H., Toyo-oka K., Wang K.H., Wettz C., Whittaker C., Wilming L., Runcitonal annotation of a full-length mouse cDNA collection."; REMBL, AK008187; Bab25519.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 EVSAPSEQGONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWF 169
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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32.8%; Score 499; DB 11; Length 310;
Best Local Similarity 37.0%; Pred. No. 5.4e-38;
Matches 117; Conservative 60; Mismatches 113; Indels 26
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SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1110002N33Rik protein.
JCAM3 OR JCAM2 OR 1110002N23RIK.
                                                                                                                                                                                                                                                                                                                                                                                  310 AA.
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STRAIN=CS7BL/6J; TISSUE=Small intestine;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
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PROSITE; PS50835; IG LIKE; 2.
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121 NLQEDKVMLEVL 132
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RESULT 7
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             MQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE----TSFQKSNSSSKA 282
                                STRAIN-CS-TBL/6J; TISSUE-Mesonephros;
STRAIN-CS-TBL/6J; TISSUE-Mesonephros;
MEDLINE-2234683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the ALD Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
AMILI-Incorp.
Nature 420:563-573(2002).
BMBL; ANJ00304; CAC20704.1; -.
EMBL; AK012156; BABL28683.1; -.
EMBL; AK032833; BAC28049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
"Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-Mar-2003 (TrEMBLrel. 25, JAM-2 (1110002N23Rik protein)
(Junction cell adhesion molecule 3).
JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
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                                                                                                                                                                                                                   310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                          295 RTSEEGDFRHKSSFVI 310
                                                                                     283 TTMSENDFKHTKSFII 298
                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
PubMed=11036763;
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Q9EPK4
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X MEDLINB-21085660; PubMed=11217851;

X MEDLINB-21085660; PubMed=11217851;

X Arakawa T., Shinagawa A., Shibata K., Komno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchl P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchl P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Marchioni L., Mashima J., Mazzarelli J., Shamoto N.,

K., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
                                                                                                                                                                                                                                                                                                                                 2
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                                                                                                                                                                                                                                                                                                                               1 MARRSRHRL-----LLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILAC-K
                                                                                                                                                                                                                                                                                                                                                        TPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKYRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 KDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                       32.8%; Score 499; DB 11; Length 310; 37.0%; Pred. No. 5.4e-38; ive 61; Mismatches 112; Indels 20
                                                                                                                                                                                             310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
111000203281k protein.
JCAM3 OR JCAM2 OR 1110002N23R1K.
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                                  Interpro; IPR007110; Ig-like.
Interpro; IPR003598; Ig_c2.
Interpro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 TTMSENDFKHTKSFII 298
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RTSEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                            Sest Local Similarity 37.09
Attches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
MGI:1933820; Jcam2
                  MGI:1933825; Jcam3
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                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                             SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOVDDLNISGIIAAVVVVALVISVCGLGVCYAORKGYF--SKE----TSFOKSNSSSKA 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MARRSRHRL-----LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILAC-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 KDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Junctional adhesion molecule 3 precursor (Junctional adhesion
molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein FLJ90828)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.,
"Heterogeneity of endothelial junctions is reflected by differential
expression and specific subcellular localization of the three JAM
family members."
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S. Hayashizaki Y.;
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-590(2001).
EMBL; AKO03326; BAB22715.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.6%; Score 496; DB 11; Length 3 37.0%; Pred. No. 1e-37; ive 61; Mismatches 112; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6692BCAD68EA4B1D CRC64;
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                                                                                                                                                                                                    MCD; MGI:1933826; JCcam2.
MCD; MGI:1933825; JCcam3.
InterPro; IPR005110; Ig-like.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
SNART; SM00408; IGC2; 1.
PROSITE; PSS0835; IG_LIKE; 2.
Immunoglobulin domain.
SEQUENCE 310 AA; 34819 MW; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 TTMSENDFKHTKSFII 298
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SEQUENCE FROM N.A.
TISSUE=Brain;
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51 -KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE--TSFQ---KSNSSS 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MALRRPPRIRICARLPDFFLILLFRGCLIG----AVNLKSSNRTPVVQ--EFESVELSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Gaps
                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 310;
                    wurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H.
Junctional adhesion molecules (JAMs) and interendothelial
                                                                                                                        SEQUENCE FROM N.A.
Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
"Characterization of Junctional Adhesional Molecule-3 on Platelets: A New Member of Immunoglobulin Superfamily.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.6%; Score 481; DB 4; Length 31
35.8%; Pred. No. 2.5e-36;
tive 60; Mismatches 116; Indels
                                                                               Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 30 POTENTIAL.
310 AA; 35020 MW; CE39ADF33EA1DAB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Junction adhesion molecule 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 YIRTDEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY:
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
SEQUENCE FROM N.A. Aurrand-Lions M.A.
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al protein.
300 AA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.
                                                                                                                                                                                                                                                                                                                             191
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  STREENERS
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                                                                                                                                                                                                                                                                                                                                                                                                         RCEVSAPSEQGONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 -KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE--TSFQ---KSNSSS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 98
                                                                                                             "Narrowing the critical region within 11q24-qter for hypoplastic left heart and identification of a candidate gene, JAM3, expressed during cardiogenesis.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                              1 MARRSRHRL-----LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILAC
                                                                                                                                                                                                                                                                                                                            Gaps
Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                 31.6%; Score 481; DB 4; Length 355; 35.8%; Pred. No. 3e-36; ive 60; Mismatches 116; Indels
                                                                                                                                                                                                                                                               JUNCTION ADHESION MOLECULE 3. 8B1577DEA7B1D4F8 CRC64;
                                                       Hearn T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010690; AAH10690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 AA,
                                                                                                                                                         EMBL; AJ416101; CAC94776.1; ...
Genew; HGNC:15532; JAM3.
InterPro; IPR007110; 19-1ike.
InterPro; IPR003598; 1g.c2.
InterPro; IPR003006; 1g_MHC.
FABM; PR0047; 1g; 2.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 KATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YIRTDEEGDFRHKSSFVI 355
                                                                                                                                                                                                                                                                           SEQUENCE 355 AA; 39602 MW;
                                                                                                                                                                                                                                                                                                                       Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
            Mammalia; Eutheria;
NCBI_TaxID=9606;
 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                     SEQUENCE FROM N.A.
                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
                                                                                                                                                                                                                                                                                                                                                                                                                                        108
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096FL1
AC 096FL
DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-MA
DE HYPOC.
OC MAMMAT OC MAMMAT OC NX NCBI
RN 121
RN 121
RP SEQUE
RC TISSU
RA STRAU
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127 TLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGSQST 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 RSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 VLAVLALITLGICCAYRRGYFINNKQDGESYRNPGKPDGVNYIRTDEEGDFRHKSSFVI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 VALVISVCGLGVCYAQRKGYF--SKE--TSFQ---KSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,70 full-length cDNBs.";
Nature 420:563-573 (2002).
EMBL; BC021876; AAH21876.1; -.
EMBL; AK033574; BAC28369.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig-MfC.
InterPro; IPR003596; Ig-V.
FAGM; PR0047; ig; 2.
SMART; SM00406; IG-X.
PROSITE, PSS0835; IG_V: IG-X.
PROSITE, PSS0835; IG_V: IG-X.
PROSITE, PSS0835; IG_V: IG-X.
PROSITE, PSS0835; IG_V: IC-X.
PROSITE FAGM: PROPER IN-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILAC-KTPKKTVXSRLEWKKL-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.7%; Score 421; DB 11; Length 300;
                                                                                                                                                                                                                                                                                                                                                              Query Match 31.6%; Score 480; DB 4; Length 30 Best Local Similarity 36.5%; Pred. No. 3.1e-36; Matches 109; Conservative 60; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Junction cell adhesion moleculel).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                     SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32423 MW; 3CE561E8FF3B97EC CRC64;
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS5035; IG_LIKE; 2.
Hypothetical protein; Immunoglobulin domain.
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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us-09-852-797-76.rspt

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204 AFDSGEYYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLVTLILLGLLIFGIWFAYSR 263
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Kirsch T., Wellner M., Haller H., Lippoldt A.;

"Cloning of the rat junctional adhesion molecule (JAM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 AA; 28122 MW; FE38521A911582D0 CRC64;
                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Junction adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Junctional adhesion molecule (Fragment).
                                              GYF---SKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                       264 GYFERTKKGTAPGKKVIYSQPSARSEGEFKQTSSFLV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.9%; Score 393.5; DB 4 36.9%; Pred. No. 2.6e-28; ive 41; Mismatches 97
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Matches 87; Conservative
                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                              265
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                                                                                                                                                           RESULT 13
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                                                                                                                                                                                                                                                                   KKL-GRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLE 122
                                                                                                                                                                                EDITVILEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLG 182
                                                                                                                                                                                                                                                                                                                                                                                                                     241 IAAVVVVALVISVCGLGVCYAQRKGYF---SKETSFQKSNSSSKATTMSENDFKHTKSFI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 AEMIDFNIRIKNVIRSDAGKYRCEVSAPSEQGQNLEEDIVTLEVLVAPAVPSCEVPSSAL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 VIFSSSGITFSSVTRKDNGEYTCMVS--EDGGQNYGEVSIHLTVLVPPSKPTVSIPSSVT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQS-TNSSYTMNTKTGTLQFNTVS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 KLDTGEYSCEARNSVG-YRRCPGKRMQVDDLNISGIIAAVVVALVISVCGLGVCYAQRK 264
                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
                                                                                          4 RSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEW
                                                                                                                                                                                                                                                                                                                               SQS-TNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVG-YRRCPGKRMQVDDLNISGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFSSP-----CYNNQITVPYADR
                         12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.9%; Score 409.5; DB 11; Length 300; 34.3%; Pred. No. 1e-29; ive 49; Mismatches 98; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Sprague Dawley;
Mashima H., Kojima I.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF276998; AAF78250.1;
InterPro; IPR007110; Ig-like.
R InterPro; IPR003006; Ig-MHC.
R InterPro; IPR003596; Ig-V.
R Ffam; PR00047; Ig: 2.
R SMART; SM00406; IGV; 1.
R PROSITE; PS50835; IG-LIKE; 2.
SEQUENCE 300 AA; 32369 MW; 45AE362A96158BFA CRC64;
34.6%; Pred. No. 8.9e-31;
tive 55; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Junctional adhesion molecule JAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
Best Local Similarity 34.6%
Matches 104; Conservative
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Best Local Similarity 34...
Best Local Similarity 54...
The 95, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
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69 SVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 SYTMNTKIGILQFNTVSKLDIGEYSCEARNSVGYRRCPGK-RMQVDDLNISGIIAAVVVV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                             SEQUENCE FROM N.A.

Liu Y., Nugrat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M.,
Foley C., Parkos C.A.

Foley C., Parkos C.A.

"Human junctional adhesion molecule is expressed by polarized columnar
epithelia and regulates tight junction resealing.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AFIS4005, AAD43794.1;
InterPro; IPR007110; 1g-1ike.
InterPro; IPR003598; 1g_c2.
InterPro; IPR003006; 1g_MHC.
Ffam; PF00047; 1g, 2.
SMART; SM00408; 1Gc2; 1.
FROSITE: PS06915; 1G_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 SCAYSGFSSPRAASYEDRVTFLPTGITFKSVTREDTGTYTCMVF--EEGGNSYGEVKVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 ALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKA----TTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YTIDPKSGDLVFDPVSAFDSGEYYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLVTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KKLGRSVSFVYYQ-QTLQG-DFKNR--AEMIDFN--IRIKNVTRSDAGKYRCEV- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 NIFQAKSONQETVFFYQNGQSLSGPSYKNRVTAAMSPGNATITISNMQSQDTGIYTCEVL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.9%; Score 227; DB 13; Length 318;
29.1%; Pred. No. 9.6e-13;
.ive 39; Mismatches 107; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Chretien I., Robert J., Marcuz A., Garcia-Sanz J.A., Courtet M., Du Pasquier L.; Robert J., Marcuz A., Garcia-Sanz J.A., Courtet M., Du Pasquier L.; a novel molecule specifically expressed on the surface of cortical thymccytes in Xenopus.";
Eur. J. Immunol. 26:780-791(1996).
R EMBL; U43330, AAC58899.1; -.
R InterPro; IPR003100; Ig_like.
R InterPro; IPR003100; Ig_like.
R InterPro; IPR00310; Ig_like.
R Ffan; PF00047; Ig; 2.
R Pfan; PR00409; IG; 2.
R PROSITE; PS50835; IG LIKE; 2.
C SEQUENCE 318 AA; 34429 MW; 6231D24B0B806C09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 LVISVCGLGVCYAQRKGYF---SKETSFQKSNSSSKATTMSENDFKHTKSFII 298
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CTX.

Senopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.

NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databages.
EMBL, AF241241, AR641299.1; -.
InterPro: 187007110; 1g-11ke.
InterPro: 187007110; 1g-22.
InterPro: 187003106; 1g_MHC.
Pfam; PF00047; 1g, 1l.
SMART; SM00408; 1Gc2; 1.
SMART; SM00408; 1Gc2; 1.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                           SEQÜENCE 173 AA; 18706 MW; 3EE3ECDFA5AFB8B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.7%; Score 315.5; DB 11; Best Local Similarity 38.7%; Pred. No. 2.6e-21; Matches 67; Conservative 36; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 AA
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STRAIN-ff; TISSUE-Thymus;
MEDLINE-96210130; PubMed-8625968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Conservative
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1091664
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AC 09166
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AAW75220 standard; Protein; 298 AA
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1059.408 Million cell updates/sec
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2. |SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1981.DAT:*
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8. |SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1991.DAT:*
9. |SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2001.DAT:*
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1 MARRSRHRLILLILRYYVA.....SSKATTMSENDFKHTKSFII 298
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1107863 seqs, 158726573 residues
                                                                                                                                                                                                                   December 9, 2003, 17:26:03
                                                                                                                                                OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                       Perfect
                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human appropries	Hilman Gone of a con	Human dene 25 enco	Himan peorteted are	Human secreted pro	Himan gene 162 one	Secretary dence	Himan tinotional a	Human polypeptide
ΩI		AAE26983	AAE27121	ABR47926	ABU64994	ABR00172	AAW85457	AAU00512	ABP61801
DB	19	23	23	24	24	24	19	22	23
% Query Match Length DB	298	298	298	298	298	298	298	298	298
% Query Match	99.3	99.3	99.3	99.3	99.3	99.3	80.5	80.5	80.5
Score	296	296	296	296	296	296	240	240	240
Result No.		73	m	4	Ŋ	9	7	80	σ

Human junctional a	Human PRO245 prote	A33 related antige	Amino acid sequenc	Human PRO245 prote	Human PRO245 prote		Human PRO245 polyp	Human immune respo		Human PRO245 prote	Human angiogenesis	Novel human secret	Human PRO polypept	Human secreted/tra	Human A-33 related	Human PRO polypept	Human secreted/tra	Human secreted pro		Human secreted/tra	Human secreted/tra	Human polypeptide	Angiogenesis prote	Human confluency r	Human EST encoded	polype		human	l human	Novel human diagno
AA016452	AAY08060	AAY23324	AAY13354	AAB33421	AAB24401	AAY70668	AAU12339	AAU00821	AAB80222	AAB50904	AAB53081	ABU69632	ABU71455	ABU71901	ABU07738	ABU66737	ABU67013	ABU67355	ABU59818	ABU64509	ABUS4357	AAM41947	AAB70500	AAB27277	AAM23693	AAM40161	ABG22341	ABG22338	ABG22339	ABG22340
24	20	20	70	21	21	21	22	22	22	22	22	24	24	74	24	24	24	24	24	24	24	22	22	21	22	22	22	22	22	22
298	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	312	222	215	213	303	107	388	140	69	99
80.5	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	74.5	72.1	61.4	55.7	35.9	29.9	24.5	23.2	17.1
240	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	222	215	183	166	101	83	73	69	51
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40

ALIGNMENTS

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostete; obseivy; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm. Human secreted protein encoded by gene 25 clone HTEEB42. Location/Qualifiers 'label= unknown /label= unknown 97US-0040710. 97US-0040762. 97US-0048100. 98WO-US04858. 97US-0068368. (first entry) Misc-difference Misc-difference Homo sapiens. 12-MAR-1998; WO9840483-A2 14-MAR-1997; 14-MAR-1997; 30-MAY-1997; 17-SEP-1998 19-DEC-1997; A CANAL AND A CANA

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Ruben SM,
                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                       (LIHH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (MEIX/)
                                                                                                                                                                                                                                                                                                                                                                                      KYAW/)
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                                                                                                                                                                                                                                                                                                                                                                                               FISC/
                                                                                                                                                                                                                                                                                                                                                          ROSE/
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  This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate clone detailed in the descriptor line. The gene can be used to generate busion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic acid sequences: AAV3286-V3435; amino acid sequences AAW75196-W75335) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 28 polymucleotides. based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
                                                                                                                                              Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                          Length 298;
                                                                             Greene JM, Kyaw H;
Ruben SM, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Score 296; DB 19; L
Pred. No. 2.5e-273;
                                                                                                                                                                                                                                                                                                                                                                  99.3%; Scor.
100.0%; Pred. No. 4...
'... 0; Mismatches
                                                                                                                                                                                     Claim 1; Page 168-169; 201pp; English.
                                                                            CL, Gentz RL,
PA, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE26983 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                    (see AAV34286 for described uses)
97US-0048189.
97US-0048357.
97US-0050934.
97US-0048970.
97US-0057765.
                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                            298; Conservative
                                                                            Fischer (
                                                                                                                   WPI; 1998-520811/44.
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                Young PE,
                                                                                                                                                                                                                                                                                                                                                      298 AA;
                                                                                                                           N-PSDB; AAV34310.
                                      05-SEP-1997;
  30-MAY-1997
                     30-MAY-1997
                             06-JUN-1997
                                                                            Ferrie AM,
Li H, Li Y
                                                                                      Li H, Li
Wei YF,
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
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Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.

13-DEC-2002 (first entry)

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AAD44616-AAD44676 represent cDNAs corresponding to 28 human secreted protein genes, and AAE26959-AAE26999 represent the proteins they encode. AAE27000-AAE27025 represent human secreted protein fragments or their variants. The secreted proteins and genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed and include developing products for the diagnosis or treatment of immunodeficiencies, e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies, autoimmune disorders e.g., systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune themolytic anaemia, Goodpasture's syndrome, thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer; Grave's disease; diabetes mellitus; hematopoietic disorder; stroke; respiratory disorder; asthma; allergy; gastrointestinal disorder; inflammatory bowel disease; halvergenerative disorder; hepatitis; parknon's disease, Alzheimer's disease; cardiovascular disorder; atherosclerosis; myocarditis; renal disorder; fungicide; virucide; hyperproliferative disorder; acute glomerulonephritis; tonsilitis; respiratory disorder; hinitis; sinusitis; neurological disease; endometriosis; vasotropic; valnerary; cytostatic; nootropic; cardiant; anti-HIV; tranquilliser; gout; antiparasitic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted polypeptides and polynucleotides for diagnosing, preventing, treating immune, hyperproliferative, cardiovascular, neurological, reproductive disorders and identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
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Wei Y, Moore PA, Young PE, Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Human mature secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Encoded by TSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Unknown
/note= "Encoded by GWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..22
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 186; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2001; 2001US-0852659.
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Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LI H.
SOPPET D R.
GENTZ R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISCHER C L.
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ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-598780/
N-PSDB; AAD44660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZENG Z.
KYAW H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2002
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Ferrie AM;
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including septic shock, sepsis, reperfusion injury, inflammatory bowel disease, crohn's disease, haematopoietic disorders, respiratory disease, asthma and allergy, gastrointestinal disorders e.g., inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and breast), central nervous system (CNS) disorders e.g., serkinson's disease and Alzheimer's disease, AIDS-related dementia and prion disease, cardiovascular disorders e.g., myocarditis, arrhythmias, prion disease, cardiovascular disorders e.g., hepatitis, gout, tranma, pancreatitis, sarcoidosis and alogenic transplant rejection, blood-related disorder (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative disorders, respiratory disorders e.g. rhinitis, hyperproliferative disorders, respiratory disorders, pneumonitis, renal disorders. e.g. acute glomeralomephritis, neurological diseases, liver disorders. e.g. andocrine disorders e.g., hyperthyroidism, Addison's disorders e.g. endometriosis. The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LEWKKLGRSVSFVYYQQTLQGDFRNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.3%; Score 296; DB 23; Length 29
100.0%; Pred. No. 2.5e-273;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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AAE27121 standard; Protein; 298 AA
                                                                                    (first entry)
                                                                                    13-DEC-2002
                                                       AAE27121;
RESULT 3
             AAE2712:
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Human; secreted protein; autoimmune disease; hyperproliferative disorder; rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis; cerebral ischaemia; cardiovascular disorder; nervous system disorder; cardiac arrest; Alzhaimer's disease; ocular disorder; wound healing; infection; corneal infection; skin aging; food additive; preservative; tissue regeneration; immunosuppressive; antiproliferative; cycostatic; cardiant; vasorropic; cerebroprocective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.

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1..22
/label= Signal_peptide
23..298
/note= "Mature human secreted protein"
Location/Qualifiers
                                          Protein
           Peptide
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Homo sapiens

wulnerary.

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Li Y, Zeng Z, Kyaw H, Fischer CL, Li F
Wei Y, Moore PA, Young PE, Greene JM;
      /note= "Encoded by GWG"
58
                          /note= "Encoded by TSC"
     /label= Unknown
                    /label= Unknown
                                                        11-MAY-2001; 2001US-0853161.
                                                                   02-FEB-2001; 2001US-265583P.
                                                                                                                                                           Rosen CA,
Gentz RL,
                                                                                            ZENG Z.
KYAW H.
FISCHER C L.
                                                                                                                            WEI Y.
MOORE P A.
YOUNG P E.
GREENE J M.
FERRIE A M.
                                                                                                                                                                                 WPI; 2002-574454/61.
N-PSDB; AAD44878.
                                                                                                                  SOPPET D R.
                                                                             RUBEN S M.
ROSEN C A.
LI Y.
                                                                                                                       GENTZ R L.
Misc-difference 42
               Misc-difference
                                    JS2002076756-A1
                                              20-JUN-2002
                                                                                                                                                            Ruben SM, Soppet DR,
                                                                                                                                                                 Soppet DR,
Ferrie AM;
                                                                                                                                 (MOOR/)
(YOUN/)
(GREE/)
(FERR/)
                                                                              RUBE/)
                                                                                                        FISC/)
                                                                                                             LIHH/)
                                                                                                                   SOPP/)
                                                                                                  KYAW/)
                                                                                                                        GENT/)
                                                                                                                              (MEIY/)
                                                                                        (LIYY/
                                                                                             ZENG/)
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New nucleic acid molecules encoding 28 human secreted proteins, useful for diagnosing, preventing, treating or ameliorating medical conditions and as food additives or preservatives

Claim 11; Page 186-187; 209pp; English.

AAD44854-AAD44984 represent CDNAs corresponding to 28 human secreted protein genes, and AAE27097-AAE27137 represent the proteins they encode. AAE27184 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Secreted protein sequences of the invention are useful for the cliagnosis or treatment of disorders such as autoimmune diseases (e.g. cherapy. Secreted protein sequences of the invention are useful for the disorders or liver), cerebrovascular disorders (e.g. cerebral ischaemia, angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous system disorders (e.g. Alzheimer's disease), infections caused by fungi, bacteria and viruses and ocular disorders (e.g. corneal infection). The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, correspondent inpid, protein, carbohydrate, vitamins, minerals, coffectors and other nutritional components. They can also be used as food additives or preservative to increase or decrease storage capabilities, and other nutritional components. The present sequence represents a human and a protein, et al. secreted protein of the invention.

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DB 23; Length 298;
                                     99.3%; Score 296; DB 23; Length 2 100.0%; Pred. No. 2.5e-273; ive 0; Mismatches 0; Indels
                                     Query Match
Best Local Similarity 100.
Matches 298; Conservative
  298 AA;
Sequence
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9
                                               9
1 MARRSKHRLILLILRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                        1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
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0; Gaps

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241
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                                                                                                                                                                                                                          Sequence
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(ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The
proteins and their coding sequences are useful for the preparation of a
diagnostic or pharmaceutical composition for diagnosing or treating a
cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,
cardiovascular disorders, muscular disorders, reproductive disorders,
immune system disorders, pulmonary disorders, reproductive disorders,
c gastrointestinal disorders, pulmonary disorders, renal disorders,
c proliferative disorders and/or cancerous diseases and conditions, for
c wound healing and epithelial call proliferation, to treat inflammation or
c infection, for treating thrombosis and arteriosclerosis, for treating or
c preventing neural damage which occurs in neuronal disorders or
neurodegenerative conditions such as Alzheimer's disease and Parkinson's
c neurodegenerative or conditions such as Alzheimer's disease and parkinson's
c disease, to enhance bone and periodontal respeneration and aid in tissue
c transplants or bone grafts, to prevent skin aging or hair loss, to
stimulate growth and differentiation of haematopoietic cells and bone
marrow cells when used in combination with other cytokines, to maintain
                                                                                                                                    180
                                                                             120
                                                                                                                                                           241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                     241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
                                                               LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
                                                                                                                              LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
                                                                                                                                                                                                                                           LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; SEQ ID 817; 1881pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein, SEQ ID 817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR47926 standard; Protein; 298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-277340P.
19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-2002; 2002WO-US09785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-129429/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200295010-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR47926;
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                                                                                                                                                                                                                                        181
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CCCCCCCCCCCCCCCX8X4144X8X41X8X8X8X8X8X8X8X8X8X8X8X8X8X

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61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                       121 LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRCCPGKRMQVDDLNISGI
                                                                                                                                                                                                                                                                                                           1 MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
organs before transplantation or for supporting cell culture of prime
tissues, to increase or decrease differentiation or proliferation of
embryonic stem cells, or to modulate mammalian characteristics or
                                                                                                                                                                                                                                                                  Gaps
                                                                                      Note: The sequence data for this patent was published in electronic format and is available from WIPO at
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                                                                                                                                                                                                                99.3%; Score 296; DB 24; Length 298; 100.0%; Pred. No. 2.5e-273; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; immunodeficiency; multiple sclerosis;
                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein gene 25, protein.
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97US-040762P.
97US-048100P.
97US-048189P.
97US-048357P.
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                                                                                                                                                                                                                                                             Matches 298; Conservative
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                            298 AA;
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30-MAY-1997;
30-MAY-1997;
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The invention relates to an isolated polypeptide comprising an amino acid grequence at least 95% identical to sequence of 28 human secreted form, protectins, their fragment, polypeptide domain epitope, secreted form, concluded are the encoded sequence included in Arc 97921 and 97922. Also included are the encoding mucleic acids, recombinant vectors, host cells, antibodies, and genes. CT he proteins and mucleic acids are useful for diagnosing, preventing, concluded in Arc 67921 ameliorating a medical condition e.g. immunodeficiencies, severe combined immunodeficiencies, severe combined immunodeficiencies, autoimmune immunodeficiencies, severe combined immunodeficiencies, autoimmune characteries, autoimmune haemolytic anaemia, disorders (as orders, inflammatory bowel lases, crohn's disease), celerosis autoimmune haemolytic anaemia, demartitis, respiratory disorders (e.g. gastric, ovarian, lung, bladder, liver and breakling indivory, inflammatory bowel disease, crohn's disease), crespiratory disorders (e.g. gastric, ovarian, lung, bladder, liver and breakling and prinn disease), cancers (e.g. gastric, ovarian, lung, bladder, liver and breakling and prinn disease, and largy), gastrointestinal confusion injury, nother and breakling and prinn disease, cancers (e.g. parkinson's disease and Alzheimer's disease, AlDS-related disorders (misorders (e.g. parkinson's disease and Alzheimer's disease, AlDS-related charentia, and prinn disease), cardiovascular disease, and cardiopulmonary pancreatities, mycorders (thrombosis, arterial thrombosis, acterial thrombosis, cardiovascular disease, and cardiopulmonary pancreatities, sarcoidosis, dermatitia, allogenic transplant rejection), hyperpitierations, inflammation (e.g. hepetities) and cardiopulmonary complement adisorders (e.g. endometries) and disorders (e.g. endometries) are also useful to enhance or inhibit comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human secreted polypeptides and polynucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                 Li Y, Zeng Z, Kyaw H, Fischer CL, Li Wei Y, Moore PA, Young PE, Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 186; 209pp; English.
 97US-050934P.
97US-048970P.
97US-057765P.
                                                    97US-068368P.
2001US-265583P.
98WO-US04858.
                                                                                                         98US-0152060
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Gentz RL,
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KYAW H.
FISCHER C L.
                                                                                                                                                                                                                                                                                    (GENT/) GENTZ R L.
(WELY/) WEL Y.
(MOOR/) MOORE P A.
(YOUN/) YOUNG P E.
(GREE/) GREENE J M.
(FERR/) FERRIE A M.
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SOPPET D R.
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Α.Ψ.
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ROSEN
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02-FEB-2001;
12-MAR-1998;
                06-JUN-1997;
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Ferrie AM;
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(FISC/)
                                                                                                                                             (RUBE/)
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LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                              61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGON
capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           181 LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
                                                                                                                                                                                            1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
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                                                                                                                      99.3%; Score 296; DB 24; Length 298; 100.0%; Pred. No. 2.5e-273; ive 0; Mismatches 0; Indels (
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13-NOV-2001; 2001US-331287P.
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                                                                                                                                                        Matches 298; Conservative
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                                                                                                                                          Local Similarity
                                                                                       298 AA
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N-PSDB; ABZ71351.
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                                                                                         Seguence
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       ABZ71190-ABZ71478 represent CDNAs corresponding to 178 human secreted

Drotein genes, and ABP00011-ABP00299 represent the proteins they encode.

ABZ71479-ABZ714740 represent human secreted protein genomic fragments. The
invention also encompasses antibodies specific for the secreted proteins,
the use of the secreted proteins in drug screening, and recombinant

Consider and host cells comprising a nucleic acid of the invention. The
secreted proteins, nucleic acids encoding them, antibodies or antibody
fragments specific for the secreted proteins, and modulators of protein

Consephagus, stomach, small intestine, large intestine, liver, biliary
coesophagus, stomach, small intestine, large intestine, liver, biliary
tract and pancreas, and include cancers of these organs and tissues. The
coesophagus and their nucleic acids may also be used in the
treatment of immune disorders, inflammation, inflection,
hyperproliferative disorders, and to promote wound healing. Nucleic acids

Contract invention may be used for chromosome identification, chromosome
mapping, in gene therapy, for identifying individuals from minute

Consequence in arkein sequence represents a human secreted protein of the
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tissue growth activity; activin; inhibin activity; chemotactaxis;
chemokinetic activity; haemostasis; thrombolytic activity; receptor;
ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
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                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                         Sequence
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Matches
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                                                                                                                                                                                                                                          New polynucleotides encoding secreted human proteins - derived fro human foetal brain, adult brain, foetal kidney, placenta or adult pineal gland cDNA libraries.
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                                                                                                                Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Junctional adhesion protein; JAM2; cellular localisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 240; DB 19; L
Pred. No. 5.2e-220;
                                                                                                              McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human junctional adhesion protein (JAM2).
                                                                                                         Lavallie ER,
Treacy M;
                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 73-74; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.5%; Scc.
100.0%; Pred
0; M
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98US-0044466.
97US-0822167.
                                                               (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                         J, Jacobs P
Spaulding 1
                                                                                                                                                                             WPI; 1998-609890/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 298 AA
                                                                                                                                                                                                  N-PSDB; AAV82780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crohn's disease.
19-MAR-1998;
21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                              Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAY-2001
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es 240;
                                                                                                                                   Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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us-09-852-797-76.olig30.rag

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The polynuclectide encoding the polypeptide is useful for recombinant production of JAM-2 protein, which in turn is useful for recombinant of antibodies. The antibodies may be used for probing cellular localisation and/or expression of JAM2 in tissues under normal and disease states, for immunopracipitating JAM2 in cissues to determine whether it is modified by glycosylation and phosphorylation, and for determining JAM2 function. The antibodies inhibit interaction of JAM2 with inflammatory cells or influences their paracellular migration, and is therefore useful for alleviating inflammatory diseases such as arthritis, asthma, rheumatory diseases such as arthritis, asthma, rheumatorid arthritis, inflammatory bowel disease and Crohn's disease.
                                                                                                                                                                                                                                                                                      The sequence represents a human junctional adhesion molecule 2 (JAM2).
                                                                                                                                                                                                                                        Novel nucleic acids encoding human junctional adhesion protein useful for producing antibodies that are suitable for therapeutic purposes
        'note= "Possible signal peptide #1"
                          'note= "Possible signal peptide #2"
                                                   79. 298
/note= "Possible mature JAM2 #2"
                                            "Possible mature JAM2 #1"
                                                               /note= "Possible mature JAM2
237..254
/note= "Transmembrane domain"
                                                                                                                                                                                           Cunningham S, Trindad Arrate Barros M;
                                                                                                                                                                                                                                                                     Claim 4; Page 46-47; 51pp; English.
                                                                                                                                                                          (TEXA-) TEXAS BIOTECHNOLOGY CORP.
                                                                                                                                     23-AUG-2000; 2000WO-US23158.
                                                                                                                                                       99US-0150459
                                   21..298
/note= "E
                                                                                                                                                                                                              WPI; 2001-218425/22.
                                                                                                                                                                                                                                                                                                                                                                                                            298 AA;
                                                                                                                                                                                                                      N-PSDB; AASO0512
                                                                                                  WO200114404-A1
                                                                                                                                                        24-AUG-1999;
                                                                                                                    01-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                  Peptide
                                   Protein
                                                      Protein
                                                                       Domain
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ONLEEDTVTLEVLVAPPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
                                                                                                                            PRIGSQSTINSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
                                                                                                                                                                                    GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                         SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                              Gaps
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                           0; Indels
80.5%; Score 240; DB 22; L
100.0%; Pred. No. 5.2e-220;
iive 0; Mismatches 0;
                           Matches 240; Conservative
              Local Similarity
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ABP61801 standard; Protein; 298 AA

RESULT 9 ABP61801 ID ABP XX AC ABP

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ABP61801;

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04-OCT-2002 (first entry)
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Human polypeptide SEQ ID NO 155.

Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; notropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidibactic; antiadsthmatic; antiallergic; immunostimulant; antiparastic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.

Homo sapiens.

US2002065394-A1.

30-MAY-2002.

22-DEC-2000; 2000US-0745763.

98US-0040963. 18-MAR-1998;

JACOBS K.

(JACO/)

MCCOY J M.
LAVALLIE E R.
COLLINS-RACIE L A. (MCCO/)

EVANS C. MERBERG D. (EVAN/) (MERB/)

TREACY M. SPAULDING V. (TREA/) (SPAU/)

Evans C; Collins-Racie LA, LaVallie ER, Spaulding V; McCoy JM, Treacy M, Jacobs K, Mu

WPI; 2002-582343/62. N-PSDB; ABQ92017.

Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis

Claim 54; Page 116-117; 284pp; English.

Length 298;

Query Match

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The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic caid (CDNA) inserts (II), where the protein is substantially free from cother mammalian proteins. (I) are useful for preventing, treating or other mammalian proteins. (I) are useful for preventing, treatment or meablorating a medical condition, cell differentiation, antiinflammatory, cytokine, cell proliferation, cell differentiation, antiinflammatory, cytokine, cell proliferation, cell differentiation, antiinflammatory, cytokine, cell proliferation, cell differentiation, antiinflammatory, cytokine. (I) can be used to manipulate stem cells in culture to give crise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimment disease, accidental damage or cells damaged by illness, autoimment disease, accidental damage or cells damaged by illness, the proliferation of neural cells and central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Muntington's disease, amyotrophic central aclerosis. (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disease, platelet disorders such as thrombocytopaenia cor lymphoid cell disorders, platelet disorders such as thrombocytopaenia cor lymphoid cell disorders, platelet disorders such as thrombocytopaenia cor lymphoid cell disorders, platelet disorders such as thrombocytopaenia cor lymphoid sepenatation of bone, cartilage, tendon, ligament and/or nerve corpusions in tissue repeair, healing of burns, incissions, ulcers, for treating osteoporosis, osteoarthritis, bone degeneration or cegeneration and treatment of lung or liver in verient lissues, various immune deficiencies and disorders including auctoinmune disorders e.g. multiple sclerosis, rheumatoid arthritis,

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Homo sapiens.
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18-SEP-1997;
28-OCT-1997;
12-NOV-1997;
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                                                                                                                                                                                                   QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
                                                                                                                                                                                                                                          PRLGSQSTNSSYTWAYKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
                                                                                                                                                                                                                                                                        GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                    Human; gene therapy; extracellular region; junctional adhesion molecules; hubJM: immune system disorder; immune deficiency; autoimmune disorder; inflammatory disorder; cancer; wound healing; cardiovascular disease; full-length membrane-bound huJAM protein.
diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention.
                                                                                                                                                SKLEWKKLGRSVSFVYYQQTLGGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEGG
                                                                                                                                                                                                                          PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                   59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New extracellular human junctional adhesion molecule (huJAM) polypeptide, useful for treating an immune system disorder such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Extracellular domain; Specifically claimed
                                                                                                                 ö
                                                                                           Length 298;
                                                                                                               IndelB
                                                                                       80.5%; Score 240; DB 23; I. Ilarity 100.0%; Pred. No. 5.2e-220; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                        Human junctional adhesion molecule 2 (huJAM2)
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Mature huJAM2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                     AAO16452 standard; protein; 298
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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/note= ":
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                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELIL ) LILLY & CO
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                                                                   298
                                                                                       Query Match
Best Local Simi
Matches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                   Sequence
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                                                                                          The invention comprises the DNA and protein sequences of the extracellular region of human junctional adhesion molecules (huJAM). The extracellular huJAM DNA and protein sequences are useful in the treatment of: immune system disorders (e.g. immune deficiency); autoimmune disorders; inflammatory disorders; cancer; wound healing; or a cardiovascular disease. The present amino acid sequence represents the full-length membrane-bound huJAMZ protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inflammatory cell infiltration; immune response; T cell proliferation; anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; c.ell-mediated disease; spondyloarthropathy; scherosis; renal disease; inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis; diabetes mellitus; demyelinating polymeuropathy; Gulllain-Barre syndrome; multiple sclerosis; polymeuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermanitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; tramsplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human.
                                                                                                                                                                                                                                                                                                                                                                                                             SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRLGSQSTNSSYTMYTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLN1S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIIAAVWVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
                                                                                                                                                                                                                                                                                                                                                                                      SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                                                                                                                                                                                                                                 Gaps
immune deficiency or an inflammatory disorder, cancer, wound healing
                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                      Length 298;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0%; Pred. No. 5.2e-220; Matches 240; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      80.5%; Score 240; DB 24;
                                                       Disclosure, Fig 1; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY08060 standard; Protein; 312
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97US-0059263.
97US-0065186.
97US-0066364.
97US-0066770.
                   a cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO245 protein.
                                                                                                                                                                                                                                                               298 AA;
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24-NOV-1997;
04-JUN-1998;
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AAY23324 standard; Protein; 312 AA.

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carrier or excipient), a novel processor containing (appart from a carrier or excipient), a novel processor containing (appart from a carrier or excipient), a novel processor of infiltration of infiltration of infiltration. The composition increase or decreases any of the effects (inflammatory cells into tissue; (ii) an immune response; or (ii) To proliferation. The composition increases or decreases any of the effects (inflammatory cells include their fragments, are used to treat immune-related diseases, and their fragments, are used to treat immune-related diseases.

CC and their fragments, are used to treat immune-related diseases, particularly T cell-mediated diseases. The diseases treated include systemic spondyloarthropathies, systemic sclerosis (scleroderma), inflammatory myopathies (stematomyositis, polympositis), dispathic inflammatory myopathies (stematomyositis, polympositis), dispathic inflammatory myopathies, systemic vasculitis, sarcoidosis, autoimmune thrombocytopenia, indipathic inflammatory myopathies (dermatomyositis, polympositis), hemoglobinuria), autoimmune thrombocytopenia, indipathic antematical thrombocytopenia, indipathic antematical thrombocytopenia, indipathic antematical thrombocytopenia, indipathic antematory demyelinating polymeuropathy, inflectious hepatitis active hepatitis, tubulointersitial mediated renal disease, clinflammatory demyelinating polymeuropathy, inflectious hepatitis, and sclerosing cholangitis, inflammatory bowel diseases including chaptains of molangitis, inflammatory bowel diseases including chaptains and sclerosing cholangitis, inflammatory bowel diseases including chaptains and sclerosing cholangitis, inflammatory bowel diseases. Culcerative colitis; atopic dermatitis, and sclerosing cholangitis, inflammatory demyelinating polymeuropathy, inflammatory demyelinating polymeuropathy, inflammatory demyelinating polymeuropathy, inflammatory demyelinating polymeuropathy, inflammatory demyelinating polymeuropathy.

Culcerative colitis; crohn's disease, erythema multi
                                                                                                                                                                                                                                                                                            This invention describes a novel composition containing (apart from a
                                                                                                                                                                             or
                                                                                                                                                                        Composition containing novel polypeptide PRO245, its agonist
                                                   Wood WI;
                                                   Tumas D,
                                                                                                                                                                                                                                                Example 1; Fig 2; 177pp; English.
                                                   Gurney AL,
(GETH ) GENENTECH INC
                                                 Goddard A,
                                                                                             WPI; 1999-229499/19
                                                                                                                       N-PSDB; AAX37664
                                                                                                                                                                                               antagonist
                                                 Fong S,
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312 AA; Sequence

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118
                                                          QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
                                                                                                     PRLGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
                                                                                                                                                           PRLGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
                                          SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                         Gaps
                           ;
0
                                                                                                                                                                                   GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
                                                                                                                                                                                                 77.2%; Score 230; DB 20; Length 312; 100.0%; Pred. No. 1.8e-210;
                      0; Indels
      100.0%; Pred. ....
                    Matches 230; Conservative
           Similarity
                                             59
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RESULT 12 AAY23324

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The specification describes A33 related antigens PR0301, PR0362 and PR0245. The methods and compositions of the invention are useful for the treatment and diagnosis of inflammatory disease and tumours in mammals. Such inflammatory diseases include of inflammatory bowel disease, systemic slerosis, soleroderma, clupus erythematosis, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic selerosis, soleroderma, cliopathic inflammatory myopathies, systemic selerosis, soleroderma, cliopathic inflammatory myopathies, systemic selerosis, autoimmune hemolytic slogren's syndrome, systemic vaculitis, sarcoidosis, autoimmune hemolytic canemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria, autoimmune thrombocytopenia, thyroiditis, Grave's disease, autoimmune thrombocytopenia, thyroiditis, Grave's disease, cleania, immune pancytopenia, lidopathic thyroiditis, atrophic thyroiditis, diabetes mellitus, immune-mediated thrombocytopenia, lymphocytic thyroiditis, atrophic thyroiditis, diabetes mellitus, immune-mediated sensitiis, inflammatory solicitis, inflammatory solicitis, incommune chronic active cliopathic polyneuropathy, hepatobiliary diseases, infectious hepatitis, octive cholangitis, inflammatory and fibrotic lung diseases, alteria, esensitive enteropathy, Whipple's disease, autoimmune chronic active cholangitis, inflammatory and fibrotic lung diseases allergic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis
cransplantation associated disease disease. The present sequence
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                                                                                                                                              related antigen; PRO301; PRO362; PRO245; inflammatory disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney AL, Napier MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigens PRO301, PRO362 and PRO245 related to A33
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Tumas D, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 11; 122pp; English.
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98US-0078936.
                                                                                                                                                                                                                                                                                                                     98WO-US24855.
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                                                                                                           A33 related antigen PRO245.
                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                   20-NOV-1998;
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    179 PRIGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
                   238
           179 PRLGSQSTNSSYTWNTKTGTLQFNTVSKLDTGBYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                               Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                      GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
                                                                                                                   Amino acid sequence of protein PRO245
                                                                             Ā
                                                                             AAY13354 standard; Protein; 312
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9708-0059119.
9708-00591219.
9708-0059121.
9708-0059184.
9708-0059263.
9708-00622125.
9708-0062214.
9708-0063120.
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                                                                                                       (first entry)
                                                                                                                                                                                     Homo sapiens
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18-SEP-1997;
18-SEP-1997;
17-OCT-1997;
24-OCT-1997;
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24-OCT-1997;
24-OCT-1997;
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29-OCT-1997;
31-OCT-1997;
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28-OCT-1997
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AAY13344-403 represent secreted and transmembrane human proteins.

The cDNA sequences are obtained from cDNA libraries, prepared from

CC fetal lung, fetal lidner, fetal brain,

CT the encoded polypeptides have specific uses based on their retina.

The encoded polypeptides have specific uses based on their homology to

Known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

CC known polypeptides, e.g. PRO211 and intenance of gastrointestinal

CC with the preservation and maintenance of gastrointestinal

CC uterration and congenital microvillus atrophy, skin diseases associated

With abnormal keratinocyte differentiation (e.g. psoriasis, epithelial

CC uterration and congenital microvillus atrophy, skin diseases associated

With abnormal keratinocyte differentiation (e.g. psoriasis, epithelial

CC ptent effects on cell growth and development, diseases related to

CC growth or survival of nerve cells including Parkinson's disease,

CC growth or survival of nerve cells including Parkinson's disease,

CC for fibromodulin, e.g. for reducing dermal scarring. PRO266 can be used as a

CC usher Syndrome or Atrophia areats; PRO533 may be used in the treatment

CC uther Lumombotic agent; PRO287 polypeptides and portions may have

CC therefore a papications in wound healing and tissue repair; PRO317 can

CC be used for treating problems of the kidney, uterus, endometrium, blood

Verseels, or related tissue, e.g. in the heart of genital tract.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney AL, Pennica D,
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                                                                           970S-0065186.
970S-0065846.
970S-006583.
970S-0066120.
970S-0066772.
970S-0066770.
                              97US-0064248.
97US-0064809.
97US-0064103
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Best Local Similarity
Matches 230; Conserv
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                                                                           12-NOV-1997;
17-NOV-1997;
18-NOV-1997;
21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
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24-NOV-1997;
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GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288

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Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemacological; antiarthritic; antirheumatic; immunosuppressive; antianaemic; hepatotropid; antidabetic; nootropic; neuroprotective; antianaemic; hepatotropid; virucide; antipooriatic; antiallargic; antiathmatic; systemic lupus erythematosus; rheumatoid arthritis; antianaemic; spondyloarthropathy; systemic sclerosis; sprondyloarthropathy; systemic sclerosis; thyroiditis; didopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaemia; immune-mediated renal disease; hepatoblilary disease; Mihipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immuno-mediated skin disease; allergic disease; munological disease; transplantation associated disease;
                                                                        Human PRO245 protein UNQ219 SEQ ID NO:36
 AAB33421 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                                              99WO-US05028.
99US-0123618.
99US-0123957.
99US-0125775.
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99US-0131445.
99US-0132371.
99US-0134287.
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2000WO-US00376.
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                                               (first entry)
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                                               29-JAN-2001
                                                                                                                                                                                                                                                                                   Homo sapiens
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10-MAR-1999;
12-MAR-1999;
23-MAR-1999;
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30-NOV-1999;
01-DEC-1999;
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30-DEC-1999
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                        AAB33421;
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(GETH) GENENTECH INC

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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and disagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vasculitis, aarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin disease, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACS8379 to AACS879 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACS879 to AACS842 and sequences given in the exemplification of the present invention.
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                                                                                                                   Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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P, Goddard A, Gurney AL, Hebert C, H
an J, Pennica D, Shalton DL, Smith V;
Watanabe CK, Wood WI, Yan M;
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                                                                                                                                                                                        Claim 33; Fig 16; 309pp; English.
                  Pan J,
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Baker KP,
                  , Lu Y, Pa
Tumas D,
                                                                      WPI; 2000-572271/53.
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                                                                                      N-PSDB; AAC58586
                Kabakoff RC,
                                    Stewart TA,
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useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB2438E to AAB24435 represent nucleotide and protein sequences used in
                                                                                                                                                                                                                                                                                                                                                                          Gerber H, Hillan KJ, Goddard A;
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial angiogenic disorders in mammals -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.2%; Score 230; DB 21; L 100.0%; Pred. No. 1.8e-210; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                         Ferrara N,
Klein RD, F
I, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 72; Fig 28; 315pp; English.
                                                                                                                                                                                                                                                              99WO-US21094.
99WO-US21090.
99WO-US21547.
                                                                                                                                                                                           99US-0141037.
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Gurney AL, Kl
Williams PM,
                                                                                                                        99WO-US05028.
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99WO-US20111.
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Les 230; Conservative
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N-PSDB; AAA77562.
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Godowski PJ, G
Watanabe CK, W
 WO200032221-A2
                                                                                                                                                                             02-JUN-1999;
23-JUN-1999;
20-JUL-1999;
                                                                                                                       08-MAR-1999;
12-MAR-1999;
28-APR-1999;
14-MAY-1999;
                                                                                                                                                                                                                      26-JUL-1999;
01-SEP-1999;
08-SEP-1999;
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15-SEP-1999;
15-SEP-1999;
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29-OCT-1999;
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118 QNLEEDTVTLEVLVAPPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178

PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238

119

179 179

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PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238

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Perfect score:

Title:

Run on:

Sequence:

Scoring table:

Word size :

Searched:

Minimum DB Maximum DB

Database :

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; Sequence 9, Application US/09254465A; Patent No. 6410708
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Best Local Similarity 100.
Matches 298; Conservative
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Sequence 9, Appli
                                                                                                                                     December 9, 2003, 17:34:36; Search time 15.5749 Seconds (without alignments) 809.548 Million cell updates/sec
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                                                                                                                                                                                                                                                                298
1 MARRSRHRLLLLLLRYLVVA.....SSKATTMSENDFKHTKSFII 298
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Sequence 76, Application US/09152060

Patent No. 6448230

Patent No. 6448230

PAPLICANT: Rosen et al.

APPLICANT: Rosen et al.

ITILE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1.US

CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT FILING DATE: 1998-09-11

EARLIER FILING DATE: 1998-03-12

EARLIER FILING DATE: 1997-03-14

EARLIER APPLICATION NUMBER: 60/040,762

EARLIER APPLICATION NUMBER: 60/040,710

EARLIER FILING DATE: 1997-03-14

EARLIER APPLICATION NUMBER: 60/050,934

EARLIER APPLICATION NUMBER: 60/040,710

EARLIER APPLICATION NUMBER: 60/040,710
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US-09-254-465A-9
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                                                                                              OM protein - protein search, using sw model
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seq length: 200000000
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312 4
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296

Result No.

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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Goddard, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: 099-03-05
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1997-11-21
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
DOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (58); COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-152-060-76
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100.0%; Pred. No. 8.9e-276;
tive 0; Mismatches 0;
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VET: 2.0
EARLIER FILING DATE: 1997-12-19
SEQ ID NO 76
LENGTH: 298
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
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PRIOR APPLICATION NUMBER: US 60/078,936;
PRIOR FILING DATE: 1998-03-20;
PRIOR APPLICATION NUMBER: PCT/US98/19437;
PRIOR FILING DATE: 1998-09-17;
NUMBER OF SEQ ID NOS: 30;
SEQ ID NO 9;
LENGTH: 312;
TYPE: PRT
CORGANISM: Homo sapiens
                                                                                                                                      ; ORGANISM: Hom
US-09-254-465A-9
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298
1 MARRSRHRLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
                              GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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			Description		Sequence 76. Appl			Sequence 30, Appl		Sequence 2. Appli	Sequence 64. Appl	Sequence 64. Appl		Seguence 9. Appli	64	64	64. 7	Sequence 64, Appl	
SUMMAKIES			ID	US-09-853-161-76	US-09-852-659A-76	US-09-852-797-76	US-09-745-763-38	US-09-799-777-30	US-10-139-849-2	US-10-192-791-2	US-09-909-320-64	US-09-909-088B-64	US-09-905-291A-64	US-09-953-499-9	US-09-902-853-64	US-09-907-824-64	US-09-907-841-64	US-09-904-011-64	
			DB	0	6	10	0	0	15	16	10	10	10	10	10	10	10	11	
		Query	Length	298	298	298	298	298	298	298	312	312	312	312	312	312	312	312	
	ąp.	Query	Match	99.3	99.3	99.3	80.5	80.5	80.5	80.5	77.2	77.2	77.2	77.2	77.2	77.2	77.2	77.2	
			Score	296	296	296	240	240	240	240	230	230	230	230	230	230	230	230	
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Sequence 64, Appl Sequence 64, Appl	
16 230 77.2 312 11 US-09-906-742-64 18 230 77.2 312 11 US-09-906-838-64 20 230 77.2 312 11 US-09-907-613-64 21 230 77.2 312 11 US-09-907-613-64 22 230 77.2 312 11 US-09-904-859-64 23 230 77.2 312 11 US-09-904-859-64 24 230 77.2 312 11 US-09-904-850-64 25 230 77.2 312 11 US-09-904-850-64 26 230 77.2 312 11 US-09-906-646-64 27 230 77.2 312 11 US-09-906-646-64 28 230 77.2 312 11 US-09-906-646-64 29 230 77.2 312 11 US-09-906-966-64 30 230 77.2 312 11 US-09-907-786-64 31 230 77.2 312 11 US-09-907-786-64 32 230 77.2 312 11 US-09-907-786-64 33 230 77.2 312 11 US-09-907-956-64 34 230 77.2 312 11 US-09-907-956-64 35 230 77.2 312 11 US-09-907-956-64 36 230 77.2 312 11 US-09-907-956-64 37 230 77.2 312 11 US-09-907-956-64 38 230 77.2 312 11 US-09-907-656-64 39 230 77.2 312 11 US-09-907-656-64 40 230 77.2 312 11 US-09-907-556-64 41 230 77.2 312 11 US-09-905-556-64 42 230 77.2 312 11 US-09-905-566-64 43 230 77.2 312 11 US-09-905-576-64 44 230 77.2 312 11 US-09-905-576-64 45 230 77.2 312 11 US-09-905-576-64 46 230 77.2 312 11 US-09-905-576-64 47 230 77.2 312 11 US-09-905-576-64 48 230 77.2 312 11 US-09-905-576-64 49 230 77.2 312 11 US-09-905-576-64 49 230 77.2 312 11 US-09-905-576-64 40 230 77.2 312 11 US-09-905-576-64 41 230 77.2 312 11 US-09-905-576-64	RESULT 1 US-09-853-161-76 Sequence 76, Application US/09853161 Sequence 76, Application US/09853161 Sequence 76, Application US/09853161 GENERAL INFORMATION: TITLE OF INVENTION: 28 Human Secreted Proteins TITLE OF INVENTION: 28 Human Secreted Proteins TITLE OF INVENTION: 28 Human Secreted Proteins CURRENT REDICATION NUMBER: US/09/853,161 CURRENT FILING DATE: 2001-05-11 PRIOR APPLICATION NUMBER: 00/126,583 PRIOR PRILING DATE: 1998-09-11 PRIOR PRILING DATE: 1998-09-11 PRIOR FILING DATE: 1998-09-11 PRIOR FILING DATE: 1997-03-14 PRIOR FILING DATE: 1997-03-14 PRIOR PRILING DATE: 1997-05-30 PRIOR PRILING DATE: 1997-05-30 PRIOR PILING

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             FEATURE:
NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (58)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-853-161-76
                                                                                                                                                                                                                                                                                                                                                                                 61 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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                                                                                                                                                                                                              Length 298;
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                                                                                                                                                                                                           Query Match 99.3%; Score 296; DB 9; Le Best Local Similarity 100.0%; Pred. No. 2.5e-269; Matches 298; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR PLING DATE: 1997-06-30
PRIOR PLING DATE: 1997-06-06
PRIOR PLING DATE: 1997-06-06
PRIOR PRIOR OF SEQ ID NOS: 121
SOFTWARE: PALENTIN VEY: 2.0
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ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: SITE
LOCATION: (42)
OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
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Sequence 76, Application US/09852797
GENERAL INFOMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PSO03P2
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-14
PRIOR PILING DATE: 1997-03-14
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PRIOR PILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-07-07-07
PRIOR PILING DATE: 1997-06-06
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PRIOR PILING DATE: 1997-07-07
PRIOR PILING DATE: 1997-07-07-07
PRIOR PILING DATE: 1997-07-07
PRIOR PILING DATE: 1997-
TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (58)
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US-09-799-777-30
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                                                                                                      NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                      ; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-797-76
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Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                               Length 298;
                                                                                                                                                                                                                                             99.3%; Score 296; DB 10; Length 29
100.0%; Pred. No. 2.5e-269;
iive 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
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APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <UNKNOWN>
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Patent No. US2002065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
LAVAIIE, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 298
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.'
Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
COUNTRY: U.S.A.
                                                                   ORGANISM: Homo sapiens
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
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Hillman, Jennifer L.
Corley, Nail C.
Goaley, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                80.5%; Score 240; DB 9; Length 298; 100.0%; Pred. No. 8.5e-217;
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MEDIUM TYPE: Rloppy disk
MEDIUM TYPE: Rloppy disk
MEDIUM TYPE: Rloppy disk
OMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATE: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION: cUnknown>
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ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               100.0%; Preq. ....
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APPLICATION NUMBER: US/09/002,485
                                                                                                                                                                          STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-745-763-38
                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09799777 Patent No. US20020091244A1 GENERAL INFORMATION:
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STATE: CALIFORNIA
COUNTRY: USA
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Best Local Similarity 100.0
Matches 240; Conservative
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/139,849
FILING DATE: 07-May-2002
FILING DATE: 07-May-2002
ATTORNON DATA:
APPLICATION NUMBER: US/09/643,929
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENČE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza.
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cunningham, Sonia
APPLICANT: Cunningham, Sonia
Barros, Maria Pia
TITLE OF INVENTION: A UNCTIONAL ADHESION PROTEIN (JAM 2
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                             Query Match 80.5%; Score 240; DB 9; Le Best Local Similarity 100.0%; Pred. No. 8.5e-217; Matches 240; Conservative 0; Mismatches 0;
                                                                                                                                                                                                          LIBRARY: DUODNOTO2
CLONE: 1704050
SEQUENCE DESCRIPTION: SEQ ID NO: 30
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEPHONE: (650) 855-0555
                                                                                       LENGTH: 298 amino acida
TYPE: amino acid
STRANDEDNESS: single
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                   TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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Publication No. US20030079238A1
GENERAL INFORMATION:
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                                                                                                                                                             TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 60601
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Sequence 2, Application US/10192791
Publication No. US20030130166A1
Publication No. US20030130166A1
ADDICATION:
TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (J)
FILE REFERENCE: TEX492P0430
CURRENT APPLICATION NUMBER: US/10/192,791
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                              80.5%; Score 240; DB 15; Length 298; 100.0%; Pred. No. 8.5e-217; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.5e-217;
Live 0; Mismatches 0; Indels
                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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SEQ ID NO 2
LENGTH: 298 amino
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Best Local Similarity 100.0
Matches 240; Conservative
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ORGANISM: Homo sapiens
US-10-192-791-2
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Best Local Similarity
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; MOLECULI
; SEQUENCI
US-10-139-849-2
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US-09-909-320-64
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118

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59 SRLEWKYLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                             SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/909,088B CURRENT APPLICATION NUMBER: US/09/909,088B CURRENT FILING DATE: 2001-07-18

PRIOR FILING DATE: 2001-07-18

PRIOR FILING DATE: 2005-02-2

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 64, Application US/09909088B Patent No. US20020146709A1
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Botstein, David
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Eaton, Dan L.
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US-09-909-088B-64
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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77.2%; Score 230; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 230; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
FRIOR APPLICATION NUMBER: PCT/USO/04414
FRIOR APPLICATION NUMBER: PCT/USO/04414
FRIOR FILING DATE: 1999-07-07
FRIOR FLING DATE: 1999-07-07
FRIOR FLING DATE: 1999-07-26
FRIOR FILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-09-08
FRIOR FLING DATE: 1999-09-08
FRIOR FLING DATE: 1999-09-13
FRIOR FLING DATE: 1999-09-15
FRIOR FLING DATE: 1999-10-05
FRIOR FLING DATE: 1999-11-29
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FRIOR FLING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30916
PRIOR PRILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                             Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Gerritsen, Mary E.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-909-320-64
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APPLICANT:
APPLICANT:
APPLICANT:
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US-09-953-499-9
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Pred. No. 2.1e-207;
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100.0%; Pred. No. 2.....
0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Patent No. US20020160374A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J.
Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Goddard, A.
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Paoni, Nicholas F.
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Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Best Local Similarity 100.
Matches 230; Conservative
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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US-09-905-291A-64
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APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Mary A.

APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Wapier, Mary A.

APPLICANT: Wapier, Mary A.

TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT

TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS

TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS

TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS

CURRENT APPLICATION NUMBER: US/09/953,499

CURRENT FILING DATE: 1999-03-05

PRIOR PRICH APPLICATION NUMBER: PCT/US98/24855

PRIOR APPLICATION NUMBER: US 60/066,364

PRIOR PRICH APPLICATION NUMBER: US 60/066,364

PRIOR FILING DATE: 1999-03-20

PRIOR FILING DATE: 1999-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

SEQ ID NO 9

**CHARACTERICANTED NO SEC ID NOS: 30

**CHARACTERICANTED NO SEC ID NOS: 30

**CHARACTERICANTED NO SEC ID NOS: 30
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Publication No. US20020192659A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Hillan, Kenneth, J
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APPLICANT: ABhkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Bestoin, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hangeter
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Matches 230; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Kljavin, Ivar J. Mather, Jennie P.

Pan, James

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toy, Margaret Annitewart, Timothy A. Umas, Daniel
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Matches 230; Conservative
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PLILING DATE: 2000-02-22
PRIOR PLILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-07-8
PRIOR PLILING DATE: 1999-07-8
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-8
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Grimaldi, Christopher J.
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Sequence 64, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Eaton, Dan L.
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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-64
                                                                                                                               Query Match
Best Local Similarity
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A APPLICANY: Williams, Daniel
A APPLICANY: Williams, Deniel
A APPLICANY: Wood, William, I
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 1046-62.
CURRENT APPLICATION: NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/663.350
PRIOR APLICATION NUMBER: 05/0143.048
PRIOR APLICATION NUMBER: 05/0143.048
PRIOR FILING DATE: 1999-07-28
PRIOR APLICATION NUMBER: US 60/145.698
PRIOR APLICATION NUMBER: US 60/146.222
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21049
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2091
PRIOR PELING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/2091
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1000-01-05
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Grimaldi, Christopher J.
                                               Sequence 64, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Hillan, Kenneth,
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                                      Gaps
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77.2%; Score 230; DB 10; Length 312; 100.0%; Pred. No. 2.1e-207; ative 0; Mismatches 0; Indels (
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                        Gaps
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 423
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                                                                                                                                                                                                                                                                                     Length 312;
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                                                                                                                                                                                                                                                                                   77.2%; Score 230; DB 10; L
100.0%; Pred. No. 2.1e-207;
iive 0; Mismatches 0;
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CURRENT PELLING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665, 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 64, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 230; Conservative
                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                       ; OKGANISM: no:
US-09-907-841-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-904-011-64
                                                                                                                                                                             SEQ ID NO 64
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119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLEN 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. NC.
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-904-011-64
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

December 9, 2003, 17:33:14; Search time 14.5366 Seconds (without alignments) 1971.458 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-852-797-76 298 1 MARRSRHRLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298

OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

283308 segs, 96168682 residues Searched:

30

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Π Query Score Match Length DB Result

Description

No matches found

Search completed: December 9, 2003, 17:38:31 Job time : 14.5366 secs

```
GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model Run on:

December

9, 2003, 17:26:43; Search time 10.3833 Seconds (without alignments) 1349.666 Million cell updates/sec US-09-852-797-76 Title: Perfect score:

1 MARRSRHRLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298 Scoring table: Sequence:

127863 seqs, 47026705 residues Searched:

Gapop 60.0 , Gapext 60.0

30 Word size :

-Total number of hits satisfying chosen parameters:

ξ¢.

Maximum DB seg length: 2000000000 Minimum DB seq length: 0

Post-processing: Listing first 45 summaries

SwissProt 41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Motoditages	P57087 homo sapien
T.		240 80.5 298 1 JAM2_HUMAN
S.	1	П
Length		298
Query		80.5
sult Query No. Score Match Length DR ID		240
Result No.		ı

ALIGNMENTS

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TISSUE-Vascular endothelial cells;
MEDLINE=20317114; PubMed=10779521;
Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
"Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells.";
J. Biol. Chem. 275:19139-19145(2000).
                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Junctional adhesion molecule 2 precursor (Vascular endothelial
Junction-associated molecule) (VE-JAM).
                    298 AA
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=20507930; PubMed=10945976;
                                                16-OCT-2001 (Rel. 40, Created)
                                                                                                                                    JAM2 OR VEJAM OR C210RF43.
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
               JAM2 HUMAN P57087;
JAM2_HUMAN
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DOMAIN DISULFID DISULFID

DOMAIN

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                             ဥ
Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjercke R.J., Vanderslice P., Morris A.P., Brock T.A.;
"A novel protein with homology to the junctional adhesion molecule: Characterization of leukocyte interactions.";
J. Biol. Chem. 275:34750-34756(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- DATABASE: NAME=PROW; NOTE=PROW 2:1-3 (2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
JUNCTIONAL ADHESION MOLECULE 2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 1g; 2. SMART; SM00408; IGc2; 1. PROSITE; PS50835; IG LIKE; 2. Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 606870; -. Good of the control of the control of CO:0005887; C:integral to plasma membrane; NAS. OC:0016337; P:cell-cell adhesion; NAS. InterPro; IPR00110; Ig-11ke. InterPro; IPR001598; Ig-2: InterPro; IPR003006; Ig-MHC.
                                                                                         MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY016009; AAG49022.1; -.
EMBL; BC017779; AAH17779.1; -.
Genew; HGNC:14686; JAM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF255910; AAF81223.1; -.
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2238
2259
2298
2238
2238
2109
                                                                 SEQUENCE FROM N.A.
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DOMAIN
TRANSMEM
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FT CARBOHYD 98 98 N-LINKED (GLCNAC. ..) (POTENTIAL).
FT CARBOHYD 236 N-LINKED (GLCNAC. ..) (POTENTIAL).
FT CARBOHYD 236 N-LINKED (GLCNAC. ..) (POTENTIAL).
SQ SEQUENCE 298 AA, 33207 MW, CA708E18E22DCAEE CRC64,

Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-214;

Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118

Qy 119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPETTWFKDGIRLLEN 178

Db 119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPETTWFKDGIRLLEN 178

Qy 119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPETTWFKDGIRLLEN 178

Qy 119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPETTWFKDGIRLLEN 178

Qy 119 PRLGSQSTNSSYTWMTKGTLQFNTVSKLDTGESSCEARNSVGYRRCPGKRMQVDDLNIS 238

Qy 239 GILAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF11 298

Qy 239 GILAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF11 298
```

Search completed: December 9, 2003, 17:36:26 Job time : 11.3833 secs

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GenCore version 5.1.6
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December 9, 2003, 17:32:33 ; Search time 37.899 Seconds (without alignments) 2029.071 Million cell updates/sec
OM protein - protein search, using sw model
                                               Run on:
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US-09-852-797-76 298 1 MARRSRHRLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298 Title: Perfect score:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table: Sequence:

830525 segs, 258052604 residues

Searched:

Word size :

ħ. 0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL 23:*

1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_numan:*
5: Sp_numan:*
6: Sp_nammal:*
7: Sp_num:*
7: Sp_phage:*
8: Sp_organelle:*
8: Sp_lant:*
1: Sp_lant:*
1: Sp_rodent:*
1: Sp_virus:*
2: Sp_virus:*
3: Sp_virus:*
3: Sp_virus:*
3: Sp_virus:*
4: Sp_virus:*
5: Sp_virus:*
5: Sp_virus:*
6: Sp_virus:*
6: Sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ω Query Score Match Length DB

Result

Description

No matches found.

Search completed: December 9, 2003, 17:38:06 Job time : 53.899 secs

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9, 2003, 17:13:47; Search time 39.4564 Seconds (without alignments) 1198.803 Million cell updates/sec
                                                                                                                                                                                                                            1 MARRSRHRLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                        OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                      US-09-852-797-76
298
                                                                                                              December
                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                            Sequence:
                                                                                                            Run on:
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the and a second desired with the Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits Satisfying Chosen parameters:

1107863 seqs, 158726573 residues

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Word size :

Searched:

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Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human secreted pro- Human gene 25 enco Human secreted pro- Human secreted pro- Human secreted pro- Human gene 162 enco Secreted pro- Human junctional a Human polymenide
SUMMARIES	AAW7520 AAE26983 AAE27121 ABR47926 ABU64994 ABR00172 AAW85457 AAW606512 ABP61801
DB	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
% Query re Match Length DB I	88888888888888888888888888888888888888
% Query Match	99.3 99.3 99.3 99.3 90.8 80.8 80.8
Score	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Result No.	H 42 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16

97US-0068368. 97US-0040710. 97US-0040762. 97US-0048100.

14-MAR-1997; 14-MAR-1997; 30-MAY-1997;

Human junctional a Human DRO245 profe	lated a	Amino acid sequenc	Human PRO245 prote	Human PRO245 prote	Human PRO245 prote	Human PRO245 polyp	Human immune respo	Human PRO245 prote	Human PRO245 prote	Human angiogenesis	Novel human secret	Human PRO polypept	Human secreted/tra		Human PRO polypept	Human secreted/tra			Human secreted/tra	Human secreted/tra	Human polypeptide	Angiogenesis prote	Human confluency r	Human EST encoded			human	Novel human diagno	
AAO16452			AAB33421	AAB24401	. AAY70668		AAU00821	AAB80222	AAB50904	AAB53081		ABU71455	ABU71901	ABU07738		ABU67013	ABU67355	•	ABU64509	ABUS4357	AAM41947	AAB70500	AAB27277	AAM23693	AAM40161	ABG22341	ABG22338	ABG22339	ABG22340
298 24	312 20		12 21										12 24	312 24		312 24	12 24	7	•	312 24	•	215 22	•	•	107 22	•	140 22	~	66 22
		2	3	3	3		3		2	3			3	2				7											
80.5	77.	77.	77.	77.	77.	77.	77.	•	77.	77.	•			•		77.	77.2	77.	77.		74.	72.	61.	55.	35.	29.9	24.	23.	17.
240	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	222	215	183	166	107	8	73	69	51
10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40

ALIGNMENTS

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm. Human secreted protein encoded by gene 25 clone HTEEB42. Location/Qualifiers AAW75220 standard; Protein; 298 AA. /label= unknown /label= unknown 98WO-US04858 (first entry) Misc-difference 58 Misc-difference Homo sapiens 29-JAN-1999 WO9840483-A2 12-MAR-1998; 17-SEP-1998 AAW75220;

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Protein
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(KYAW/)
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                                                                                                                                                                                Homo
    This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate lusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. ANV34277) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic acid sequences: AAN34264-V3325; amino acid sequences AAN31646-W325; awhich are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides, based on which tissues are described for each of the 28 polynucleotides. Specific uses are described for each of the 28 polynucleotides. Specific uses are described for each of the 28 polynucleotides. Specific uses are described for each of the 28 polynucleotides. Dased on which tissues they are most highly expressed in
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                                                                                                                                                                                                      Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
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                                                                                                             Greene JM, Kyaw H;
Ruben SM, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%; Score 296; DB 19; L
100.0%; Pred. No. 2.5e-273;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                             Claim 1; Page 168-169; 201pp; English.
                                                                                                        Fischer CL, Gentz RL,
, Moore PA, Rosen CA,
ang PE, Zeng Z;
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97US-0048189.
97US-0048357.
97US-0050934.
97US-0048970.
97US-0057765.
                                                                                 GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                               WPI; 1998-520811/44.
N-PSDB; AAV34310.
                                                                                                                                     Young PE,
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298; Conserv
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                                                        05-SEP-1997;
                                           06-JUN-1997
                            30-MAY-1997
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Li H, Li Y
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Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.

(first entry)

13-DEC-2002

AAE26983

AAE26983 standard; Protein; 298 AA

RESULT 2 **AAE**26983

AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted protein genes, and AAE26959-AAE26999 represent the proteins they encode. AAE27000-AAE27025 represent human secreted protein fragments or their variants. The secreted proteins and genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed and include developing products for the diagnosis or treatment of immunodeficiencies, e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies, autoimmune disorders e.g., systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer; Grave's disease; diabetes mellitus; hematopoietic disorder; stroke; respiratory disorder; asthma; allergy; gastrointestinal disorder; inflammatory bowel disease; heurodegenerative disorder; hepatitis; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; myocarditis; renal disorder; fungicide; virucide; hyperproliferative disorder; acute glomerulonephritis; tonsilitis; respiratory disorder; rhinitis; sinusitis; neurological disease; endocrine disorder; hinitis; sinusitis; neurological disease; endocrine disorder; vulnerary; cytostatic; nootropic; cardiant; anti-HIV; tranquilliser; gout; antiparasitic. Novel human secreted polypeptides and polynucleotides for diagnosing, preventing, treating immune, hyperproliferative, cardiovascular, neurological, reproductive disorders and identifying modulators of therapeutic use Li Y, Zeng Z, Kyaw H, Fischer CL, Li I Wei Y, Moore PA, Young PE, Greene JM; 23..298 /note= "Human mature secreted protein" /label= Unknown /note= "Encoded by GWG" by TSC" 1..22 /label= Signal_peptide Location/Qualifiers Claim 11; Page 186; 209pp; English. /label= Unknown /note= "Encoded 11-MAY-2001; 2001US-0852659. 98US-0152060. Rosen CA, Gentz RL, ZENG Z. KYAW H. FISCHER C L. WPI; 2002-598780/64. SOPPET D R. GENTZ R L. Misc-difference 58 Misc-difference 42 RUBEN S M. ROSEN C A. N-PSDB; AAD44660. US2002077287-A1 11-SEP-1998; sapiens. 20-JUN-2002 Soppet DR, Ferrie AM; Ruben SM,

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LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
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including septic shock, sepsis, reperfusion injury, inflammatory bowel disease. Crohn's disease, haematopojoietic disorders, respiratory disorders e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and breast), central nervous system (CNS) disorders e.g., ischaemic brain injury and/or stroke, neurodegenerative disorders e.g., parkinson's disease and Alzheimer's disease, AIDS-related dementia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MARRSRHRILLILLIRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR 60
                                                                                                                                                           prion disease, cardiovascular disorders e.g., myocarditie, arrhythmias, atheroselerosis, inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis, sarcoidosis and allogenic transplant rejection, bloodrelated disorder (thrombosis, arterial thrombosis, atheroselerosis), hyperproliferative disorders, respiratory disorders e.g. rhinitis, sinusitis, tonslitis, lung cancer, allergic disorders, preumonitis, renal disorders. e.g. acute glomerulonephritis, neurological diseases, liver disorders, e.g. acute glomerulonephritis, neurological diseases, liver disorders, e.g. acute glomerulonephritis, neurological diseases, liver printitismi, infectious diseases and reproductive system secreted protein of the invention.
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100.0%; Pred. No. 2.5e-273;
ive 0; Mismatches 0; Indels
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Matches 298; Conservative
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Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76. AAE27121 standard; Protein; 298 AA 13-DEC-2002 AAE27121; AAE27121
1D AAEZ
XX AC AAEZ
XX XX II3-1
XX II3-1 RESULT 3

(first entry)

Human; secreted protein, autoimmune disease, hyperproliferative disorder; rheumatoid arthritis, neoplasm; cerebrovascular disorder; angiogenesis; cerebral ischaemia, cardiovascular disorder; nervous system disorder; cardiac arrest, Alzheimer's disease; ocular disorder; wound healing; infection; corneal infection; skin aging; food additive; preservative; tissue regeneration; immunosuppressive; antiproliferative; cycostatic; cardiant; vasocropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; vulnerary.

Homo sapiens.

/label= Signal_peptide Location/Qualifiers Peptide Protein

23..298 — _ _ /note= "Mature human secreted protein"

/note= "Encoded by GWG" /label= Unknown /note= "Encoded by TSC" /label= Unknown 11-MAY-2001; 2001US-0853161 02-FEB-2001; 2001US-265583P FISCHER C L. GENTZ R L. WEI Y. SOPPET D R. MOORE P A. YOUNG P E. RUBEN S M. ROSEN C A. GREENE J M. FERRIE A M. Misc-difference 42 Misc-difference 58 ZENG Z. KYAW H. US2002076756-A1 20-JUN-2002 (MOOR/) (YOUN/) (GREE/) (FERR/) (KYAW/) (FISC/) (LIHH/) RUBE/) SOPP/) GENT/) WEIY/) ZENG/)

er CL, Li H; Greene JM; Li Y, Zeng Z, Kyaw H, Fischer CL, Wei Y, Moore PA, Young PE, Greene Rosen CA, Gentz RL, Soppet DR, Ferrie AM; Ruben SM,

WPI; 2002-574454/61. N-PSDB; AAD44878.

for diagnosing, preventing, treating or ameliorating medical conditions and as food additives or preservatives New nucleic acid molecules encoding 28 human secreted proteins, useful

Claim 11; Page 186-187; 209pp; English.

AAD44854-AAD44984 represent CDNAs corresponding to 28 human secreted

Drotein genes, and AAE27097-AAE27137 represent the proteins they encode.

AEA27138-AAE27146 represent human secreted protein fragments. The genes

and their corresponding secreted proteins are useful for preventing,

treating or ameliorating medical conditions, e.g., by protein or gene

therapy. Secreted protein sequences of the invention are useful for the

diagnosis or treatment of disorders soft the invention are useful for the

chemmatoid arthritis), hyperproliferative disorders (e.g. neoplasms of

the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,

angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous

system disorders (e.g. Alzheimer's disease), infections caused by fungi,

bacteria and viruses and ocular disorders (e.g. corneal infection). The

prolypeptides can also be used to aid wound healing and epithelial cell

colypeptides can also be used to aid wound healing and epithelial cell

proliferation, to prevent skin aging due to sumburn, to maintain organs

to regenerate tissues and in chemotaxis. They can also be used as food

additives or preservative to increase or decrease storage capabilities,

fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors

and other nutritional components. The present sequence represents a human secreted protein of the invention,

298 AA; Sequence

Gaps ; 0 Length 298; 99.3%; Score 296; DB 23; Length 2: 100.0%; Pred. No. 2.5e-273; .ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 298; Conservative

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1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDOQVVTAVXYQEAILACKTPKKTVXSR 60

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The present invention relates to novel human secreted proteins

(ABR4763-ABR46145) and their coding sequences (ACC50344-ACC50856). The
proteins and their coding sequences are useful for the preparation of a
diagnostic or pharmaceutical composition for diagnosing or treating a
cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,
coronary arteriosclerosis and myocardial ischemena), neural disorders,
immune system disorders, muscular disorders, reproductive disorders,
coronary contrestinal disorders, pulmonary disorders, renal disorders,
coronary contributes and/or cancerous diseases and conditions, for
proliferative disorders and/or cancerous diseases and conditions, for
cound healing and epithelial cell proliferation, to treat inflammation or
infection, for treating thrombosis and arteriosclerosis, for treating or
coronary arteriosclerosis such as Alzheimer's disease and Parkinson's
controllerative conditions such as Alzheimer's disease and Parkinson's
controllerative or bone and periodontal regeneration and aid in tissue
conditions are an expension of hammatopoietic cells and bone
marrow cells when used in combination with other cytokines, to maintain
                                                                  LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
                                                                                     240
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                                                                                                                                                                                                                              Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
                    LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
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cardiovascular disorders such as arrhythmia -
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; rheumatoid arthritis; diabetes mellitus; hematopoietic disorder; inflammatoid arthritis; diabetes mellitus; hematopoietic disorder; inflammatoid disorder; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; lschaemlc brain injury; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; blood-related disorder; thrombosis; atherosclerosis; hyperproliferative disorder; acute glomerulonephritis; Addison's disease; endometriosis; infectious disease; reproductive system disorder; wound repair; angiogenesis; lymphatic disorder; vaccine; wound repair; hair colour; human.
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organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism.
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                                                         Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                   Length 298;
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100.0%; Pred. No. 2.5e-273;
ive 0; Mismatches 0;
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97US-040762P.
97US-048100P.
97US-048189P.
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Best Local Similarity 100.C
Matches 298; Conservative
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30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
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97US-048970P.
97US-057765P.
97US-068368P.
2001US-26563P.
98WO-US04858.
                               ZENG Z.
KYAW H.
FISCHER C L.
LI H.
SOPPET D R.
GENTZ R L.
MOORE P A.
YOUNG P E.
GREENE J M.
                       RUBEN S M.
ROSEN C A.
           02-FEB-2001;
     05-SEP-1997;
                 11-SEP-1998;
              12-MAR-1998
                                                        (YOUN/)
(GREE/)
(FERR/)
                                (ZENG/)
(KYAW/)
(FISC/)
                                         (LIHH/)
(SOPP/)
(GENT/)
                       RUBE/)
                          (ROSE/)
                              (LIYY/)
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Li Y, Zeng Z, Kyaw H, Fischer CL, Li I Wei Y, Moore PA, Young PE, Greene JM; Rosen CA, Gentz RL, Ferrie AM; SM Soppet Ruben

WPI; 2003-310989/30 N-PSDB; ABX96990 New human secreted polypeptides and polynucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of therapeutic use

Claim 11; Page 186; 209pp; English.

The invention relates to an isolated polypeptide comprising an amino acid gequence at least 95% identical to sequence of 28 human secreted form, proteins, their fragment, polypeptide domain, epitope, secreted form, correlated in ArCO 9721 and 97922. Also included are the encoding medical included in ArCO 9721 and 97922. Also included are the encoding nucleic acids, recombinant vectors, host cells, antibodies, and genes. Cr free proteins and nucleic acids are useful for diagnosing, preventing, crammodeficiencies, severe combined immunodeficiencies, severe combined immunodeficiencies, severe combined immunodeficiencies, severe combined immunodeficiencies, autoimmune thyroiditis, autoimmune haemolytic anaemia, industriates autoimmune thyroiditis, autoimmune haemolytic anaemia, disorders (e.g. systemic erythematosus, rheumatoid arthritis, multiple disorders (e.g. systemic erythematosus, rheumatoid arthritis, multiple coopparture's syndrome, Grave's disease, diabetes mellitus, dermatitis), heavadeopoietic disorders, inflammatory bowel disease, crohn's disease), capture in repertuain injury, inflammatory bowel disease, crohn's disease, complexity, central nervous system (CNS) disorders (e.g. septic abook, traumatic brain injury), neurodegenerative breast, cancers (e.g. gastric, ovarian, lung, bladder, liver and disorders (e.g. parkinson's disease and Alzheimer's disease, AlDS-related disorders (e.g. parkinson's disease and Alzheimer's disease, AlDS-related demenia, and prion disease), cardiovascular disease, and cardiopulmonary pancreatities, sarcoidosis, dermatitis, allogenic transplant rejection), hyperprofise, hyperprofices, e.g. edometria and disorders (e.g. edometria and disorders (e.g. edometria and disorders (e.g. edometria and disorde

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence
                                                                                                                                                                                                                                  1 MARRSRHRILLILLIRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
                                                                                                                                                                                                       1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSR
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                                                                                                                                                                    Gaps
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                                                                                                                           99.3%; Score 296; DB 24; Length 298; 100.0%; Pred. No. 2.5e-273; ive 0; Mismatches 0; Indels 0
                                                          represents a secreted protein of the invention.
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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                                                                                                                                                                      Conservative
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                                                                                                                               Query Match
Best Local Similarity
Matches 298; Conserv
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N-PSDB; ABZ71351.
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us-09-852-797-76.olig50.rag

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              AB271190-AB271478 represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. AB271479-AB2714540 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, oesophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.3%; Score 296; DB 24; L
100.0%; Pred. No. 2.5e-273;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 298; Conservative
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98WO-US05653

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The present sequence represents a secreted protein. The polynucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating e.g. as vaccines) or suppressaing activity, hematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotractic/chemokineic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cabherin/tumour invasion suppressor activity, anti-inflammatory activity, cabherin/tumour support in the specification to support these activities). The polynucleotide is also stated to be useful for gene therapy.
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                                                                                                                                                                                      New polynucleotides encoding secreted human proteins - derived fro
human foetal brain, adult brain, foetal kidney, placenta or adult
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                                                                                           MCCOY JM,
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                                                                                                                                                                                                                                                     Claim 17; Page 73-74; 113pp; English.
                                                                                         Lavallie E
Treacy M;
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                            97US-0822167.
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pineal gland cDNA libraries.
              98US-0044466
                                                           (GEMY ) GENETICS INST INC
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Best Local Similarity 100.
Matches 240; Conservative
                                                                                                          Spaulding
                                                                                                                                      WPI; 1998-609890/51.
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              19-MAR-1998;
21-MAR-1997;
                                                                                         Agostino MJ,
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04-OCT-2002 (first entry)

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The sequence represents a human junctional adhesion molecule 2 (JAM2). The polynucleotide encoding the polypeptide is useful for recombinant production of JAM-2 protein, which in turn is useful for the production of antibodies. The antibodies may be used for probing cellular localisation and/or expression of JAM2 in tissues under normal and disease states, for immunoprecipitating JAM2 protein from cells and/or stroke tissues to determine whether it is modified by glycosylation and phosphorylation, and for determining JAM2 function. The antibodies inhibit interaction of JAM2 with inflammatory cells or influences their inflammatory diseases such as arthritis, asthma, rheumatory diseases such as arthritis, asthma, rheumatoid arthritis, inflammatory bowel disease and Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids encoding human junctional adhesion protein useful for producing antibodies that are suitable for therapeutic purposes
                                               'note= "Possible signal peptide #2"
                note= "Possible signal peptide #1"
                                                                                                          /note= "Possible mature JAM2 #2"
237..254
/note= "Transmembrane domain"
                                                                               mature JAM2 #1"
                                                                                                                                                                                                                                                                                                                                          Cunningham S, Trindad Arrate Barros M;
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21..298
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                                                                                                                                                                                                                                                                                                            (TEXA-) TEXAS BIOTECHNOLOGY CORP.
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                                                                               /note= "P
29..298
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                                Peptide
                                                                Protein
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SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                       SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                  ONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLEN 178
                                                                                                                 PRIGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                                                                                      GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
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  Length 298;
                         0; Indels
80.5%; Score 240; DB 22; L
100.0%; Pred. No. 5.2e-220;
iive 0; Mismatches 0;
                         Matches 240; Conservative
             Local Similarity
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ABP61801

RESULT 9
ABP61801
ID ABP6
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AC ABP6
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the invention relates to number secreted or transmembrate protein (1), the invention relates to number secreted or transmembrane protein (1), where the protein is substantially free from acid (cDNA) inserts (II), where the protein is substantially free from the internation proteins. (I) are useful for preventing, treating or confer ammanian proteins. (I) are useful for preventing to angiogenesis. (I) exhibits activity relating to angiogenesis, or crocked proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activin or inhibin-related activities. (I) can be used to manipulate stem cells in culture to give activities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithalial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. (I) induces the proliferation of neural cells and cells that disorders (I) induces the proliferation of neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic activity, regulation of haemacropotesis and is useful for treating myeloid or lassue repair, healing of burns, incisions, ulcers, or lasue growth and in tissue repair, healing of burns, incisions or certissue growth and in tissue repair, healing of burns, incision injury contraction and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SIDI), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
                                                                          Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidibatic; antiasthmatic; antiallergic; immunostimulan; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatojid arthritis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 54; Page 116-117; 284pp; English.
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Spaulding V
                                      Human polypeptide SEQ ID NO 155.
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LAVALLIE E R.
COLLINS-RACIE L A.
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MERBERG D.
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(SPAU/)
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Evans C;

Collins-Racie LA,

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                                                                                                                                                                                                                                                                                            GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene therapy; extracellular region; junctional adhesion molecules; hubJM); immune system disorder; immune deficiency; autoimmune disorder; inflammatory disorder; cancer; wound healing; cardiovascular disease; full-length membrane-bound huJAM protein.
            such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention.
 mellitus, myasthenia gravis, allergic reactions and conditions
                                                                                                                                              59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                          GIIAAVVVVALVISVCGLGVCYAQRRGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
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                                                                                                                                                                                                                                             PRIGSOSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                                                                                                                                          New extracellular human junctional adhesion molecule (huJAM) polypeptide, useful for treating an immune system disorder such as an
                                                                                                                       Gaps
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/note= "Extracellular domain; Specifically claimed
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                                                                                                Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human junctional adhesion molecule 2 (huJAM2)
                                                                                       80.5%; scc...
100.0%; Pred. No. ...
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/label= Signal_peptide
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                                                                                       Ouery Match
Best Local Similarity 100.
Warches 240; Conservative
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N-PSDB; AAL51599.
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                                                                        298 AA;
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                                                                                                          treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Mipple's disease; skin disease; dermatitis; psoriasis asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human.
                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inflammatory cell infiltration; immune response; T cell proliferation;
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                                                                                                                                                                                                                                                             Gaps
deficiency or an inflammatory disorder, cancer, wound healing
                                                                                    extracellular region of human junctional adhesion molecules (huJAM) extracellular huJAM DNA and protein sequences are useful in the tree of: immune system disorders (e.g. immune deficiency); autoimmune disorders; inflammatory disorders; cancer; wound healing; or a cardiovascular disease. The present amino acid sequence represents tell-length membrane-bound huJAM2 protein.
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                                                                                                                                                                                                                             Length 298;
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                                                                       invention comprises the DNA and protein sequences
                                                                                                                                                                                                                             80.5%; Score 240; DB 24; L. 100.0%; Pred. No. 5.2e-220; ive 0; Mismatches 0;
                                          Disclosure, Fig 1; 131pp; English
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97US-0059263.
97US-0063186.
97US-0066364.
97US-0066364.
97US-0066370.
              cardiovascular disease
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Matches 240; Conservative
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28-OCT-1997;
12-NOV-1997;
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04-JUN-1998
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AAY23324 standard; Protein; 312 AA.

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This invention describes a movel PRO245 polypeptide (1), its agonist contrier or excipient), a novel PRO245 polypeptide (1), its agonist or antagonist, or their fragments, for modulating: (i) infiltration of inflammatory cells into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects (i) - (iii). The products of the invention have anti-inflammatory, continuorismus and anti-diabetic activity. (i), and its (ant)agonists anti-diabetic activity. (i), and its (ant)agonists and their fragments, are used to treat immune-related diseases. Continuorismus erythematosus, rheumatority, (i), and its (ant)agonists and their fragments, are used to treat immune-related diseases. Continuorismus erythematory wyopathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies, quematomyositis, polymyositis, carthritis, spondyloarthropathies, quematomyositis, sarcoidosis, autoimmune continuoria, paroxysmal nocturnal hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemolytic anemia (immune pancytopenia), thyroiditis (drave's disease, Hashimoto's thyroiditis, juvenile lymphocytopenia (didopathic thrombocytopenia), thyroiditis, atrophic thyroiditis, juvenile lymphocytopenia, multiple sclerosis, didopathic demyelinating polyneuropathy, duillain-Barre syndrome, chronic chronic active hepatitis, primary biliary cirrhosis, granulomatous (hepatitis, and sclerosing cholangitis, inflammatory bowel disease controllis; crohn's disease), autoimmune or immune-mediated skin disease including whipple's disease. Autoimmune or immune-mediated skin disease sincluding asthma, allergic thinitis, and sidease, erythema multiforme, contact dermatitis, propersensitivity, and asthma, allergic thinitis, and endiated skin disease suchic demyeliale, proprio dermatitis, contact dermatitis, promenonia, allergic dermaticis, endicated service demonia, allergic demandentiale demonia, allergic demonia addinance contact dermatitis, andipopathic demonia and demonia allergic d
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                                                                                                                                                                                                                                                                                                                                           This invention describes a novel composition containing (apart from a
                                                                                                                                                                                                  Composition containing novel polypeptide PRO245, its agonist or
                                                         Wood WI;
                                                         Tumas D,
                                                                                                                                                                                                                                                                                        Example 1; Fig 2; 177pp; English
                                                         Gurney AL,
(GETH ) GENENTECH INC
                                                      Goddard A,
                                                                                                          WPI; 1999-229499/19
                                                                                                                                        N-PSDB; AAX37664
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ö SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118 59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178 PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238 Gaps . 0 239 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288 77.2%; Score 230; DB 20; Length 312; 100.0%; Pred. No. 1.8e-210; 0; Indels 100.0%; Pred. I.C. 230; Conservative Local Similarity 312 AA; Sequence 119 59 179 Query Match 239 Best Loca Matches q ò g ઠે 셤 ò

RESULT 12 AAY23324

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treatment and disagnosis of inflammatory disease and tumours in mammals.

C treatment and disagnosis of inflammatory disease and tumours in mammals.

Such inflammatory diseases include of inflammatory bowel disease,

Such inflammatory diseases include of inflammatory bowel disease,

arthritis, spondyloarthropathies, systemic sclerosis, scleroderma,

idiopathic inflammatory myopathies, dermatomyositis, polymyositis,

Sjogren's syndrome, systemic vaculitis, sarcoidosis, autoimmune hemolytic

anemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria,

anemia, immune pancytopenia, idiopathic thrombocytopenic purpura,

immune mediated thrombocytopenia, thyroiditis, draves disease,

thyroiditis, diabetes mellitus, immune-mediated renal disease,

C Habilmoto's thyroiditis, juvenile lymphocytic thyroiditis, demyelinating diseases

CC thyroiditis, diabetes mellitus, immune-mediated renal diseases

CC thyroiditis, diabetes mellitus, immune-mediated sensitis

CC thyroiditis, mellinary cirrossis, autoimmune chronic active

CC didopathic polyneuropathy, hepatobiliary diseases, infectious hepatitis

CC D, En nonhepatocropic viruses, autoimmune chronic active

CC cholangitis, inflammatory and fibrotic lung diseases, gluten-sensitive

CC cholangitis, inflammatory and fibrotic lung diseases, gluten-sensitive

CC cholangitis, minimary bilary cirrhosis, granulomatous hepatitis

CC diseases allergic diseases of the lung such as eosinophilic pneumonias,

CC ransplantation associated diseases disease. The present sequence

CC represents provas
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                                                                                                                                                      A33 related antigen; PRO301; PRO362; PRO245; inflammatory disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney AL, Napier MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigens PRO301, PRO362 and PRO245 related to A33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 11; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                        98WO-US19437.
                                                                                                                                                                                                                                                                                                                                                                                            97US-0066364.
                                                                                                                                                                                                                                                                                                                                 98WO-US24855
                                                                                                                 A33 related antigen PRO245.
                                                                           02-SEP-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood WI;
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                                                                                                                                                                                                                 Homo sapiens.
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21-NOV-1997;
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                                      AAY23324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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97US-0064103

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RESULT 14
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                    238
PRIGSOSTNSSYTWNTKTGTLOFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
          179 PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRCCPGKRMQVDDLNIS
                                                                                                                                                                                   Zollinger-Ellison syndrome; gastrointestinal ulceration, congenital microvillus atrophy, skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                   GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
                                                                                                                                                                             Secreted protein; transmembrane protein; human; enterocolitis;
                                                                                                                                                          acid sequence of protein PRO245.
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                                                                                                  AAY13354 standard; Protein; 312
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9708-0059115
9708-0059115
9708-0059119
9708-0059121
9708-0059184
9708-0059184
9708-0052125
9708-0052125
9708-0052125
9708-0052185
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9708-0052181
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97US-0063564.
97US-0063435.
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97US-0063732.
97US-0063738.
97US-0063734.
97US-0064215.
97US-00638705.
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17-0CT-1997;
17-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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24-0CT-1997;
24-0CT-1997;
27-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
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18-SEP-1997;
18-SEP-1997;
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29-OCT-1997
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                                                                                                                     AAY13354;
179
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                                                                                  RESULT 13
AAY13354
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AAY13344-403 represent secreted and transmembrane human proteins.

CC The CDNA sequences are obtained from CDNA libraries, prepared from
fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

CC The encoded polypeptides have specific uses based on their homology to
The encoded polypeptides were specific uses based on their homology to
Known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
associated with the preservation and maintenance of gastrointestinal
CC with the preservation and chronic mucosal lesions
uccess and congenital microvillus arrophy), skin diseases associated
CC ulceration and congenital microvillus arrophy), skin diseases associated
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
CC potent effects on cell growth and development, diseases related to
CC growth or survival of nerve cells including Parkinson's disease,
CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment
CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-tumor capplications in wound healing and tissue repair; PRO317 can
CC therapeutic applications in wound healing and tissue repair; PRO317 can
CC vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and polypeptides used in, e.g. treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                         Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.2%; Score 230; DB 20; Length 312; 100.0%; Pred. No. 1.8e-210; Live 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                       Wood WI,
                                                                                                                                                                                                                                                                                     Goddard A, Gurney AL, Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig 24; 320pp; English.
                               97US-0064809
97US-0065186
97US-0065634
97US-0065634
97US-0066364
97US-0066374
97US-0066770
97US-0066770
                97US-0064248
                                                                                                                                                                                                                97US-0066453
                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal ulceration
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Best Local Similarity 100.0
Matches 230; Conservative
                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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                                 07-NOV-1997;
12-NOV-1997;
17-NOV-1997;
                                                                                   18-NOV-1997;
21-NOV-1997;
21-NOV-1997;
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24-NOV-1997;
24-NOV-1997;
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                                                                                                                                                                                                                                                                                     Chen J,
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118

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Human; immune related disease; diagnosis; antiinflammatory; cardiant;

dermatological; antiarthritic; antirheumatic; immunosupressive;

haemostatic; antithyroid; antidabetic; nootropic; neuroprotective;

antianaemic; hepatotropic; virucide; antipsoriatic; antialergic;

antiantemic; systemic lupus erythematosus; rheumatoid arthritis;

osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;

diopathic inflammatory myopathy; systemic sclerosis; sarcoidosis;

systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;

systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;

autoimmune thrombocytopaemia; immune-mediated renal disease;

inflammatory bowel disease; pluten-sensitive enteropathy;

autoimmune disease; immune-mediated skin disease; allergic disease;

y munnological disease; transplantation associated disease;

y graft rejection; graft-versus-host-disease.
                                                                   Human PRO245 protein UNQ219 SEQ ID NO:36.
AAB33421 standard; Protein; 312 AA
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99US-0123957.
99US-0125775.
99US-0128849.
99WO-US08615.
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99US-0132371.
99US-0134287.
99WO-US12252.
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99WO-US30095.
99WO-US30999.
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99US-0144758
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2000WO-US03565.
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99WO-US28409
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2000WO-US04414
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11-FEB-2000;
18-FEB-2000;
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                                             29-JAN-2001
                                                                                                                                                                                                                                                                        Homo sapiens
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04-MAY-1999;
14-MAY-1999;
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02-DEC-1999
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                       AAB33421;
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(GETH) GENENTECH INC

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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agoniets and antagonists are useful for treating and diagnosing immune related disorders. The disorders are cleated from systemic lupus erythematosus, rheumatoid arthritis, selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, Sjogren's systemic vasculitis, antoimmune haemolytic systemic vasculitis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, cutoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

Communological diseases of the lung, and transplantation probes used the isolation of human PRO sequences. AACS8579 to AACS8737 represent human PRO sequences. AACS8579 to AACS8579 to AACS8570 and protein sequences given in the exemplification of the present invention.
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                                                                                                                                                         Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                  Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W; A Y, Pan J, Pennica D, Shelton DL, Smith V; mas D, Watanabe CK, Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO245 protein sequence SEQ ID NO:67.
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Ashkenazi AJ, Baker ne,
Kabakoff RC, Lu Y, Pan
                                                                                                2000-572271/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 AA;
                                                                                                                     N-PSDB; AAC58586
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useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenicidisorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB2445s represent nucleocide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                         Gerber H, Hillan KJ, Goddard A;
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
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Klein RD, K
, Wood WI;
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                                                                                    98WO-US25108.
98US-0112850.
99WO-US05028.
99US-013357.
99US-0131445.
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99WO-US21547.
99WO-US23089.
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Gurney AL, Kl
Williams PM,
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N-PSDB; AAA77562.
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28-APR-1999;
14-MAY-1999;
02-JTN-1999;
23-JIN-1999;
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01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
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05-OCT-1999;
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Watanabe CK,
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118

PRLGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238

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Sequence 76, Appl
Sequence 9, Appli
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2: /cgn2 6/ptodata1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata1/iaa/6B_COMB.pep:*
6: /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-254-465A-9
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Maximum DB seq length: 200000000
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NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE: NAME/KEY: SITE

    i LOCATION: (58)
    j OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-76

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APPLICANT: Genencech, Inc.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Pong, Sherman
APPLICANT: Goddard, Andrey
APPLICANT: Gurney, Austin L.
APPLICANT: Wajer, Mary A.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT ITILE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS FILE REFERENCE: P1216R1(US)
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Best Local Similarity 100.0%; Pred. No. 8.9e-276;
Matches 298; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1997-11-21
               EARLIER FILING DATE: 1997-05-30
EARLIER PELING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-09-05
EARLIER PILING DATE: 1997-09-05
EARLIER PILING DATE: 1997-09-05
EARLIER PILING DATE: 1997-09-06
EARLIER PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PALENT VET. 2.0
LENGTH: 298
APPLICATION NUMBER: 60/048,357
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                                                                                                                                                                                                                                                                                                                   LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
EDGID NO 9
LENGTH: 312
TYPE: PRT
CORGANISM: Homo sapiens
US-09-254-465A-9
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APPLICATION 128 Human Secreted Proteins TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: P2003P3
FILE REFERENCE: P2003P3
FUCRENT APPLICATION NUMBER: US/09/853,161
PRIOR APPLICATION NUMBER: US/056,583
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1997-03-14
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PRIOR PILING DATE: 1997-05-30
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Sequence 76, Application US/09853161
Fatent No. US20020076756A1
GENERAL INFORMATION:
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Sequence 76, Ap
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Sequence 38, Ap
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Sequence 64, P
Sequence 9, Ag
Sequence 64, P
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-799-777-30
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US-09-909-320-64
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US-09-953-499-9
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               NAME/KEY: SITE

LOCATION: (42)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (58)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-853-161-76
                                                                                                                                                                                                                                                                                                                                                                                                                                              LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
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                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                             99.3%; Score 296; DB 9; Lv
100.0%; Pred. No. 2.5e-269;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TILLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 298; Conservative
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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PEATURE:
NAME/KEX: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659A-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 298;
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100.0%; Pred. No. 2.5e-269;
cive 0; Mismatches 0;
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Patent No. US20020172994A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P2
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CURRENT PELLING DATE: 2001-05-1

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 2001-05-1

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-03-12

PRIOR FILING DATE: 1998-03-12

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-0-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-09-05

PRIOR FILING DATE: 1997-06-06

PRIOR FILING DATE: 1997-09-05

PRIOR FILING DATE: 1997-09-05
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Best Local Similarity 100.
Matches 298; Conservative
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PRIOR FILING DATE: 1997-1:
NUMBER OF SEQ ID NOS: 118
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
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US-09-799-777-30
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                                                                                                                        CATION: (42)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEX: SITE
LOCATION: (58)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-797-76
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                                                                                                                                                                                                                                                      Length 298;
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100.0%; Pred. No. 2.5e-269;
iive 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sprunger, Suzanne A.
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Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.C
Matches 298; Conservative
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 298
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                                                                       ORGANISM: Homo sapiens
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                                                                                                           NAME/KEY: SITE
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US-09-745-763-38
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                                                      TYPE: PRT
                                                                                            FEATURE:
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238
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Hillman, Jennifer L.
Corley, Nail C.
Goaley, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                  Length 298;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIPICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                               80.5%; Score 240; DB 9; Length 29
100.0%; Pred. No. 8.5e-217;
ive 0; Mismatchës 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE
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ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
TELECOMMUNICATION INFORMATION:
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPHONE: (617) 496-8284
TELEPHONE: (617) 496-8284
TELEPHONE: (617) 876-5851
SEQUENCE CHARACTERISTICS:
TENGTH: 298 amino acids
TYPE: amino acid
STRANDEDMESS: «Unknown-
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-745-763-38
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APPLICATION NUMBER: US/09/002,485
REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30, Application US/09799777 Patent No. US20020091244A1 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: CALIFORNIA
COUNTRY: USA
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Best Local Similarity 100.0
Matches 240; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                    SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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0
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TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN
JUNCTIONAL ADHESION PROTEIN (JAM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IDOPY disk
COMPUTER: IBM PC compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
OPERATINE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/139,849
FILING DATE: 07-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/90/643,929
FILING DATE: 23-Aug-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                  80.5%; Score 240; DB 9; Le
100.0%; Pred. No. 8.5e-217;
Live 0; Mismatches 0;
                                                                                                                                                 ; CLONE: 1704050
; SEQUENCE DESCRIPTION: SEQ ID NO: 30
US-09-799-777-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
(650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10139849; Publication No. US20030079238A1; GENERAL INFORMATION: APPLICANT: Cunningham, Sonia
               TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                               LENGTH: 298 amino acida
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 312-616-5460
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                                                                                                                TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: DUODNOT02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60601
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0'
Matches 240; Conservative
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STATE: IL
COUNTRY: U.S.A.
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TELEPHONE:
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US-10-139-849-2
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US-10-192-791-2
Sequence 2, Application US/10192791
Publicatation No. US20030130166A1
Sequence 2, Application US/10192791
Publication No. US20030130166A1
GENERAL INFORMATION:
APPLICANT: Texas Biotechnology Corporation
TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (J)
FILE REFERENCE: TEX4542P0430
CURRENT APPLICATION NUMBER: US/10/192,791
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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     TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-139-849-2
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; Patent No. US20020132240A1
; GENERAL INFORMATION:
LENGTH: 298 amino
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ORGANISM: Homo sapiens
                                                                                                                                                                                         Similarity
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Best Local
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Coddard, Mail Co
                                               SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                                         119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
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                        SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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                                                                                                                                                                                                                Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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                                                                            Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: A CAIGN ENCORDING LIBE SABBLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905,291A

CURRENT PILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21091

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR PILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06
                    Acids Encoding the Same
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ORGANISM: Homo sapiens
US-09-905-291A-64
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77.2%; Score 230; DB 10; L
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 230; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PRIOR DATE: 1999-12-16
PRIOR PRIOR DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-0
PRIOR PLING DATE: 1999-12-0
PRIOR PLING DATE: 1999-12-0
PRIOR PLING DATE: 1999-12-0
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
PRIOR PRILING DATE: 1999-12-20
PRIOR PRILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Patent No. US20020160374A1
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Parent No. USZUUZZ-
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Dan L.
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Stewart, Timothy A.
Tumas, Daniel
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Wood, William, I.
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                                                                                                                                                            ONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLEN 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
Query Match 77.2%; Score 230; DB 10; Length 312; Best Local Similarity 100.0%; Pred. No. 2.1e-207; Matches 230; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09953499; Publication No. US20020182206A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Aehkenazi, Avi J.
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APPLICANT: Thins, Defined Interest Applicant: Thins, Defined Interest Applicant: Thins, Defined Interest Applicant: Thins, Defined and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/056.350
PRIOR APPLICATION NUMBER: US/09/05-18
PRIOR PILING DATE: 1000-09-18
PRIOR PILING DATE: 1999-07-06
PRIOR PELING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-09-18
PRIOR PILING DATE: 1999-09-09-18
PRIOR PILING DATE: 1999-09-09-18
PRIOR PILING DATE: 1999-09-09-18
PRIOR PILING DATE: 1999-109-18
PRIOR APPLICATION NUMBER: PCT/US99/2009-18
PRIOR APPLICATION NUMBER: PCT/US99
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                         Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-64
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                                             APPLICANT: Gurney, Austin L.

APPLICANT: Gurney, Austin L.

APPLICANT: Wary A.

APPLICANT: Wapier, Mary A.

APPLICANT: Tumas, Daniel I.

APPLICANT: Tumas, Daniel I.

APPLICANT: Tumas, Daniel I.

APPLICANT: Tumas, Daniel I.

TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS FILE REFERENCE: P1216R1(US)

CURRENT APPLICATION NUMBER: US/09/953,499

CURRENT FILING DATE: 1999-03-05

PRIOR APPLICATION NUMBER: US 60/066,364

PRIOR FILING DATE: 1999-11-21

PRIOR FILING DATE: 1999-11-20

PRIOR FILING DATE: 1999-03-05

PRIOR FILING DATE: 1999-03-05

PRIOR FILING DATE: 1999-03-07

PRIOR FILING DATE: 1999-03-07

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: US 60/078,936

PRIOR APPLICATION NUMBER: PCT/US98/19437

PRIOR APPLICATION NUMBER: PCT/US98/19437
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US-09-902-853-64

Sequence 64, Application US/09902853

Publication No. US2020192659A1

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc.
APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Goddard, A.
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                         Goddard, Audrey
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ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-64
                                                                                                                                       Query Match
Best Local Simi]
Matches 230; (
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CANT: Williams, P. Mickey
CANT: Wood, William, I.
OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,824

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: D9/665,350

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1099-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-12-0

PRIOR PILING DATE: 1999-12-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, Christopher J.
                                                  Sequence 64, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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Filvaroff, Ellen
Fong, Sherman
Goo, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                              APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
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RESULT 13
US-09-907-824-64
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                                                                                                                                                                                                                                                                                                                                   179 PRIGSOSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                                                                            119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN
                                                                     Gaps
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                      Length 312;
                                                                   Indels
                   Score 230; DB 10; L
Pred. No. 2.1e-207;
77.2%; SColl No. 2.1. 100.0%; Pred. No. 2.1. 1.00.0%; Mismatches
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CURRENT APPLICATION NUMBER: US/09/907,841

CURRENT APPLICATION NUMBER: US/09/907,841

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-18
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Grimaldi, Christopher J.
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Publication No. US20020198366A1
GENERAL INFORMATION:
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
                                                                Conservative
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Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-01-15
PRIOR PILICATION NUMBER: PCT/US99/21049
PRIOR PILICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                     Query Match 77.2%; Score 230; DB 10; Length 312; Best Local Similarity 100.0%; Pred. No. 2.1e-207; Matches 230; Conservative 0; Mismatches 0; Indels
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JENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Bresnowers, Luc
APPLICANT: Ferrara, Napoleone
'PLICANT: Ferrara, Napoleone
'PLICANT: Forg, Sherman
'ICANT: Gao, Wei-Qiang
(CANT: Gao, Wei-Qiang
(CANT: Gaowski, Paul J.
'ICANT: Godowski, Paul J.
'NT: Godowski, Paul J.
'T: Grimaldi, Christopher J.
'Hillan, Kenneth, 'T
Kljavin, Ivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 64, Application US/09904011; Publication No. US2003003530A1
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-841-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 10466-14
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
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PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-02-2
PRIOR PLING DATE: 2000-02-2
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
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PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
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PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
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ORGANISM: Homo Sapien
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

December 9, 2003, 17:21:03 ; Search time 14.5366 Seconds (without alignments) 1971.458 Million cell updates/sec

US-09-852-797-76 298 1 MARRSRHRLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298 Title: Perfect score: Sequence:

283308 seqs, 96168682 residues OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

Searched:

20 Word size :

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Post-processing: Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ü Query Score Match Length DB Result No.

Description

Search completed: December 9, 2003, 17:25:56 Job time: 14.5366 secs

No matches found

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GenCore version 5.1.6
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(without alignments)
1349.666 Million cell updates/sec
                                 ; Search time 10.3833 Seconds
                                   2003, 17:14:27
OM protein - protein search, using sw model
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                                   December
                                 Run on:
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US-09-852-797-76 Perfect score:

1 MARRSRHRLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298 Sequence:

Gapop 60.0 , Gapext 60.0 Scoring table:

127863 segs, 47026705 residues Searched:

Word size

Fotal number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	1 240 80.5 298 1 JAM2_HUMAN P57087 homo sapien
ID	240 80.5 298 1 JAM2 HUMAN
DB	
Length	298
Query Match	80.5
sult Query No. Score Match Length DB ID	240
Result No.	H

ALIGNMENTS

```
SEQUENCE FROM N.A.

TISSUE=Vascular endothelial cells;

MEDLINE=20317114; PubMed=10779521;

Palmerib D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;

"Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells.";

J. Biol. Chem. 275:19139-19145(2000).
                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Junctional adhesion molecule 2 precursor (Vascular endothelial
junction-associated molecule) (VE-JAM).
JAM2 OR VEJAM OR C21ORP43.
 298 AA
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
MEDLINE=20507930; PubMed=10945976;
 STANDARD;
                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=9606;
 HUMAN
                 P57087;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The European Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjercke R.J., Vanderalice P., Morris A.P., Brock T.A.; "A novel protein with homology to the junctional adhesion molecule: Characterization of leukocyte interactions."; J. Biol. Chem. 275:34750-34756(2000).
                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-i- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 1 immunoglobulin-like C2-type domain. DATABASE: NAME=PROW; NOTE=PROW 2:1-3(2001);
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JUNCTIONAL ADHESION MOLECULE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain; Glycoprotein; Transmembrane; Signal. SIGNAL 1 20 POTREWITAL
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IG-LIKE V-TYPE.
POTENTIAL.
POTENTIAL.
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GO; 6005887; C:integral to plasma membrane; NAS.
GO; GO:0016337; P:cell-cell adhesion; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
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EMBL; AV016009; AAG49022.1; -.
EMBL; BC017779; AAH17779.1; -.
Genew; HGNC:14686; JAMZ.
MIM; 606870; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00047; 1g; 2. SMART; SM00408; 1Gc2; 1. PROSITE; PS50835; 1G_LIKE; 2.
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us-09-852-797-76.olig50.rsp

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                                                                                                                                                                      Gaps
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98 98 N-LINKED (GLCNAC. .) (POTENTIAL)
187 187 N-LINKED (GLCNAC. .) (POTENTIAL)
236 236 N-LINKED (GLCNAC. .) (POTENTIAL)
298 AA, 33207 MW, CA78E518E22DCAEE CRC64;
                                             Query Match 80.5%; Score 240; DB 1; Length 298; Best Local Similarity 100.0%; Pred. No. 9.1e-214; Matches 240; Conservative 0; Mismatches 0; Indels
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Search completed: December 9, 2003, 17:24:01 Job time: 11.3833 secs

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GenCore version 5.1.6
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December 9, 2003, 17:20:17; Search time 32.1882 Seconds (without alignments) 2389.068 Million cell updates/sec
OM protein - protein search, using sw model
                                              Run on:
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Title: Perfect score: Sequence:

US-09-852-797-76 298 1 MARRSRHRLLLLLLLRYLVVA......SSKATTMSENDFKHTKSFII 298

830525 seqs, 258052604 residues OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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0

Post-processing: Listing first 45 summaries

Database :

sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_rvirus:* sp_bacteriap:* sp_archeap:* 89... 1111... 112... 114... 116...

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB

No. Result

Description

No matches found

Search completed: December 9, 2003, 17:25:15 Job time : 32.1882 secs

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AAW85457
                                                           9, 2003, 17:07:01 ; Search time 36.5436 Seconds (without alignments) 1198.803 Million cell updates/sec
                                                                                                                                                                                                                                                                                                 1418
1 YHKAYGFSAPKDQQVVTAVX.....SSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                        1107863
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                1107863 seqs, 158726573 residues
                                                                                                       US-09-852-797-76_COPY_23_298
                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                         Minimum DE seq length: 0
Maximum DE seq length: 200000000
         Copyright
                                                              December
                                                                                                                Perfect score:
                                                                                                                                                Scoring table:
                                       OM protein
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                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SCOXE 1415 1415 1415 1415 1414 1414 1414	Match Match 99.8 99.7 99.7	Query Query Match Length DB 99.8 298 23 99.8 298 23 99.8 298 24 99.7 298 23 99.7 298 23	DB 19 23 23 23 23 23	H	Description Secreted protein e Human junctional a Human polypeptide Human gene 25 enco
, O	1414	99.7	298	24.	ABU64994	human secreted pro Human secreted pro

10	1414	99.7	298	24	ABR00172	Human gene 162 enc
11	1399.5	98.7	303	22	AAM23693	Human EST encoded
12	1362	96.1	312	20	AAY08060	Human PRO245 prote
13	1362	96.1	312	50	AAY23324	A33 related antige
14	1362	96.1	312	20	AAY13354	Amino acid sequenc
15	1362	96.1	312	21	AAB33421	Human PRO245 prote
16	1362	96.1	312	21	AAB24401	
17	1362	1.96	312	21	AAY70668	PR0245
18	1362	96.1	312	22	AAU12339	
19	1362	96.1	312	22	AAU00821	Human immune respo
20	1362	96.1	312	22	AAB80222	Human PRO245 prote
21	1362	96.1	312	22	AAB53081	Human angiogenesis
22	1362	96.1	312	24	ABU69632	Novel human secret
23	1362	96.1	312	24	ABU71455	Human PRO polypept
24	1362	96.1	312	24	ABU71901	Human secreted/tra
25	1362	96.1	312	24	ABU07738	Human A-33 related
26	1362	96.1	312	24	ABU66737	Human PRO polypept
27	1362	96.1	312	24	ABU67013	Human secreted/tra
28	1362	96.1	312	24	ABU67355	secreted
29	1362	96.1	312	24	ABU59818	Novel secreted and
30	1362		312	24	ABU64509	
31	1362	96.1	312	24	ABU54357	Human secreted/tra
32	1356	92.6	312	22	AAB50904	Human PRO245 prote
33	1143	90.6	222	22	AAM41947	Human polypeptide
34	1139.5		388	22	ABG22341	Novel human diagno
35	1128		298	21	AAB27273	Human confluency r
36	1128	79.5	298	21	AAB27275	Murine confluency
37	1106	-	215	22	AAB70500	Angiogenesis prote
38	1092	•	213	21	AAB27277	
39	702.5	49.5	140	22	ABG22338	Novel human diagno
40	547	œ.	107	22	AAM40161	Human polypeptide
41	86.	4.	310	21	AAB27272	Human confluency r
42		4.	310	21	AAB27278	Murine confluency
43	477.5	33.7	310	21	7	Human confluency r
44	7.	m.	310	21	AAB33457	01868
45	477.5	۳.	310	21	AAY96735	PRO1868, an A33 an
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					ALLGNMENIS	
RESULT 1	-					

Secreted protein, nutritional activity, immune stimulating, vaccine, suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin, inhibin activity, chemotactaxis, chemokinetic activity, haematory, thrombolytic activity, receptor, ligand, anti-inflammatory, cadherin, tumour invasion suppressor; tumour inhibition, gene therapy. McCoy JM, Merberg D; Secreted protein encoded by clone ct864_4. Lavallie ER, Treacy M; AAW85457 standard; Protein; 298 AA. 98US-0044466. 97US-0822167. 98WO-US05653 (first entry) (GEMY) GENETICS INST INC. Agostino MJ, Jacobs K, Racie LA, Spaulding V, Homo sapiens. WO9842739-A2. 20-MAR-1998; 19-MAR-1998; 21-MAR-1997; 25-FEB-1999 01-OCT-1998. AAW85457;

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Sequence
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                                                                                                                            The present sequence represents a secreted protein. The polymucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating activity, issue avacines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activiny, haematopoiesis regulating chemotactic/chemokinetic activity, activiny, hamboly activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity (no data is given in the specification to support these activities). The polymucleotide is also stated to be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                   23 YHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEWKKLGRSVSFVYYQQTLQGD
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                                                                                                                                                                                                                                                                                                                                                                                         1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                  polynucleotides encoding secreted human proteins - derived from an foetal brain, adult brain, foetal kidney, placenta or adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Junctional adhesion protein; JAM2; cellular localisation; cellular expression; immunoprecipitation; stroke; phosphorylation; glycosylation; paracellular migration; inflammatory disease; arthritis; asthma; rheumatoid arthritis; inflammatory bowel disease; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                    99.8%; Score 1415; DB 19; Length 298; 99.3%; Pred. No. 1.6e-111; ive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Possible signal peptide #1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Possible signal peptide #2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human junctional adhesion protein (JAM2).
                                                                                                      Claim 17; Page 73-74; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                  human foetal brain, adult bra
pineal gland cDNA libraries.
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Matches 274; Conservative
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/note= "
1..28
/note= "
              WPI; 1998-609890/51
                                                                                                                                                                                                                                                                                                             298 AA
                         N-PSDB; AAV82780.
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                                                                                                                                                                                                                                                                                                             Sequence
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61 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a human junctional adhesion molecule 2 (JAM2). The polymucleotide encoding the polypeptide is useful for recombinant production of JAM-2 protein, which in turn is useful for the production of antibodies may be used for probing cellular localisation and/or expression of JAM2 in tissues under normal and disease states, for immunoprecipitating JAM2 protein from cells and/or stroke tissues to determine whether it is modified by glycosylation and phosphorylation, and for deermining JAM2 function. The antibodies inhibit interaction of JAM2 with inflammatory cells or influences their paracellular migration, and is therefore useful for alleviating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory diseases such as arthritis, asthma, rheumatoid arthritis,
inflammatory bowel disease and Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids encoding human junctional adhesion protein useful for producing antibodies that are suitable for therapeutic purposes
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Pred. No. 1.6e-111;
0; Mismatches 2;
                             29.298
/note= "Possible mature JAM2 #2"
237.254
/note= "Possible mature JAM2 #1"
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                                                                                                                             /note= "Transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (TEXA-) TEXAS BIOTECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.8%;
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Matches 274; Conservative
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ID ABP
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AC ABP
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202

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Human polypeptide SEQ ID NO 155
                                        18-MAR-1998;
                          Homo sapiens
04-OCT-2002
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                                 30-MAY-2002
                                                     (TREA/)
(SPAU/)
                                                            Merberg
                                           (JACO/)
                                                           Jacobs
                                                    MERB/)
                                                  EVAN/)
                                               LAVA/
                                                COLL/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic caid (CDNA) inserts (II), where the protein is substantially free from acid (CDNA) inserts (II), where the protein is substantially free from cother mammalian proteins. (I) are useful for preventing, treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activin or inhibin-related activities. (I) can be used to manipulate stem cells in culture to give crise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or crise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or central and peripheral nervous system diseases and neuropathies, such as creating and peripheral nervous system diseases and neuropathies, contral and peripheral nervous system diseases and neuropathies, cut activity, regulation of hamentopoiesis and is useful for treating myeloid cell disorders, platelet disorders such as thrombocytopaenia con and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, uccertion or treating osteoporosis, osteoarthritis, bone degeneration and treatment of lung or liver fibrosis, repertuation of peripheral disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
                                                                                                                      protein;
Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidabetic; antiasthmatic; antiallergic; immunostimulant; antiparastitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; setm cell; growth factor; nervous system disease; neuropathy; attentiation; adisease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evans C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Page 116-117; 284pp; English.
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Spaulding V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-2000; 2000US-0745763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0040963
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LAVALLIE E R.
COLLINS-RACIE L
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Treacy M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABQ92017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, gene therapy, extracellular region, junctional adhesion molecules,
huJAM; immune system disorder; immune deficiency; autoimmune disorder;
inflammatory disorder; cancer; wound healing; cardiovascular disease;
full-length membrane-bound huJAM protein.
                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                          82
                    such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention.
  conditions
                                                                                                                                                                                                                                                                                                                                                                               83 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                                                          23 YHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                               1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
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0
                                                                                                                                                                           Score 1415; DB 23; Length 298;
Pred. No. 1.6e-111;
0; Mismatches 2; Indels 0
mellitus, myasthenia gravis, allergic reactions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
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'label= Signal_peptide
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/note= "Mature huJAM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                        99.8%;
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Best Local Similarity 99.3
Matches 274; Conservative
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                                                                                                                                    298 AA;
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                                                                                                                                    Seguence
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                                                                                                           The invention comprises the DNA and protein sequences of the extracellular region of human junctional adhesion molecules (huJAM). The extracellular huJAM DNA and protein sequences are useful in the treatment of: immune system disorders (e.g. immune deficiency); autoimmune disorders; inflammatory disorders; cancer; wound healing; or a cardiovascular disease. The present amino acid sequence represents the full-length membrane-bound huJAM2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS, cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                          83 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                        New extracellular human junctional adhesion molecule (huJAM) polypeptide, useful for treating an immune system disorder such as an immune deficiency or an inflammatory disorder, cancer, wound healing,
                                                                                                                                                                                                                                                                                                                                         FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
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                                                                                                                                                                                                                                                                                                                                                                                                                 143 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN
                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ
                                                                                                                                                                                                                                                                                        1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                                                23 YHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                        DB 24; Length 298;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein encoded by gene 25 clone HTEEB42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                      99.8%; Score 1415; DB 24; 99.3%; Pred. No. 1.6e-111; iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW75220 standard; Protein; 298 AA
                                                                                      Disclosure; Fig 1; 131pp; English
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                                                              or a cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                     Best Local Similarity yy.s
Matches 274; Conservative
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                               298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                     Query Match
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This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino acid sequences AAV5196-W7535) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 28 polymucleotides, based on which tissues they are most highly expressed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.7%; Score 1414; DB 19; Length 298; 100.0%; Pred. No. 2e-111; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                  Greene JM, Kyaw
Ruben SM, Soppet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 168-169; 201pp; English.
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Li H, Li Y, Moore PA, Rosen CA,
Wei YF, Young PE, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (see AAV34286 for described uses).
                                                                       970S-0040710.
970S-0040762.
970S-0048100.
970S-0048189.
970S-0068187.
970S-0068937.
                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
98WO-US04858
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12-MAR-1998;
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                                                                             14-MAR-1997
14-MAR-1997
                                                                                                                                                          30-MAY-1997
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9 82 120 142 202 240

AAE26983

therapy. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed and include developing products for the diagnosis or treatment of immunodeficiencies, e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies, autoimmune disorders e.g., systemic lupus expthematosus, rheumatoid arthritis, multiple sclerosis, autoimmune the products for the diabetes menlitus, dermatitis, inflammatory conditions thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, Grave's disease, diabetes menlitus, dermatitis, inflammatory conditions including septic shock, sepsis, reperfusion injury, inflammatory bowel disease, haemacopoietic disorders, respiratory disorders e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, inflammatory bowel disease, neurodegenerative disorders e.g., ischaemic brain injury and/or stroke, neurodegenerative disorders e.g., canten neurodegenerative disorders e.g., schinson's disease, cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis, inflammatory disorders e.g., myocarditis, arrhythmias, atherosclerosis, inflammatory disorders e.g., myocarditis, arrhythmias, carded disorder (thrombosis, arterial thrombosis, atherosclerosis), hyperpoinferative disorders, respiratory disorders, permanative disorders, permanative disorders, respiratory disorders, permanative disorders, inflammatory disorders, permanative disorders, inflammatory disorders, permanative disorders, respiratory disorders, permanative disorders, allergic disorders, permanative disorders, respiratory disorders, permanative disorders, allergic disorders, allergic disorders, permanative disorders, allergic disorders, allergic disorders, allergic disorders, allergic disorders, allergic disorders, and the invention, care general respiratory, and represents and reproductive system disord

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AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted protein genes, and AAE26959-AAE26999 represent the proteins they encode. AAE27000-AAE27025 represent human secreted protein fragments or their variants. The secreted proteins and genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene
                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 186; 209pp; English.
                                                                                                                                                                                                                          (ROSE/)
                                                                                                                                                                                                                                                                  (WEIY/)
                                                                                                                                                                                                                                                             (GENT/)
                                                                                                                                                                                                                                                                                  Soppet
                                                                                                                                                                                                                                    ZENG/
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Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer; Grave's disease; diabetes mallitus; hematopoietic disorder; stroke; respiratory disorder; asthma; allergy; gastrointestinal disorder; inflammatory bowel disease; neurodegenerative disorder; hepatitis; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; myocarditis; renal disorder; fungicide; virucide; hyperproliferative disorder; acute glomerulonephritis; tonailitis; respiratory disorder; raute glomerulonephritis; tonailitis; respiratory disorder; rhinitis; sinusitis; neurological disease; endocrine disorder; Addison's disease; reproductive system disorder; anti-HIV; tranquilliser; gout; antiparasitic.
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                                                                                                                                                              Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
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Wei Y, Moore PA, Young PE, Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23..298 _____/note= "Human mature secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Unknown
/note= "Encoded by TSC"
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/note= "Encoded by GWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= Signal_peptide
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AAE26983 standard; Protein; 298 AA
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                                                                                                        (first entry)
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Gentz RL,
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SOPPET D R.
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ROSEN C A.
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WEI Y.
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KYAW H.
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                                                                                                      13-DEC-2002
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(FISC/)
(LIHH/)
(SOPP/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    99.7%; Score 1414; DB 23;
100.0%; Pred. No. 2e-111;
ive 0; Mismatches 0;
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Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          298 AA;
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Gaps

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Length 298; Indels

99.7%; Score 1414; DB 23; 100.0%; Pred. No. 2e-111;

Query Match Best Local Similarity 100.(Matches 276; Conservative

100.0%; Preu. ...

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82

61 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGONLEEDTVTLEVLVAPAVPSCEVP 120

23 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD 1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD

83 FKNRAEMIDENIRIKNVTRSDAGKYRCEVSAPSEQGONLEEDTVTLEVLVAPAVPSCEVP

SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180 143 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFN 202

121

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240

203 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 262

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181 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ

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AAD44854-AAD44984 represent CDNAs corresponding to 28 human secreted

Drotein genes, and AAE27097-AAE27137 represent the proteins they encode.

AAE27138-AAE27144 represent human secreted protein fragments. The genes
and their corresponding secreted proteins are useful for preventing,
treating or ameliorating medical conditions, e.g., by protein or gene
creating or ameliorating medical conditions, e.g., by protein or gene
creating or ameliorating medical solding, e.g., by protein or gene
chargy. Secreted protein sequences of the invention are useful for the
diagnosis or treatment of disorders such as autoimmune diseases (e.g.
therapy. Secreted protein sequences of the invention are useful for the
diagnosis or treatment of disorders (e.g. cerebral ischaemia,
crheumatoid archiris), hyperproliferative (e.g. cerebral ischaemia,
crheumatoid archiris), hyperproliferative (e.g. cerebral ischaemia,
candidenesis, candiso be used to aid wound healing and epithelial cell
proliferation, to prevent skin aging due to sunburn, to maintain organs
before transplantation, for supporting cell culture of primary tissues,
corrected tissues and in chemotaxis. They can also be used as food
additives or preservative to increase or decrease storage capabilities,
fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
and other nutritional components. The present sequence represents a human
creaments.
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nucleic acid molecules encoding 28 human secreted proteins, useful diagnosing, preventing, treating or ameliorating medical conditions as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
Wei Y, Moore PA, Young PE, Greene JM;
                                                                                   'note= "Mature human secreted protein"
                                                                                                                               note= "Encoded by GWG"
                                                                                                                                                                       /note= "Encoded by TSC"
                                                     /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 186-187; 209pp; English
                           Location/Qualifiers
                                                                                                                                                           /label= Unknown
                                                                                                                /label= Unknown
                                                                                                                                                                                                                                                            11-MAY-2001; 2001US-0853161
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Gentz RL,
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ZENG Z.
KYAW H.
FISCHER C L.
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N-PSDB; AAD44878.
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ROSEN C A.
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WEI Y.
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FERRIE A M.
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                                                                                                Misc-difference
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Homo sapiens
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(ROSE/)
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(LIHH/)
(SOPP/)
(GENT/)
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(FERR/)
                                       Peptide
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(YOUN/)
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Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, arcentaged received and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, upulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases and conditions, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia -
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                                                                                                   Human secreted protein, SEQ ID 817.
ABR47926 standard; Protein; 298 AA
                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
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                                                                12-JUN-2003
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                                 ABR47926;
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298 AA;

9703-040762P.
9703-040189P.
9703-048189P.
9703-0481357P.
9703-0481970P.
9703-048765P.
9703-057765P.
200103-255583P.
96800-USQ4858

06-JUN-1997

19-DEC-1997

30-MAY-1997

30-MAY-1997 30-MAY-1997 30-MAY-1997

11-MAY-2001; 2001US-0852797

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wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in 'neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or half loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                          Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 2e-111;
ive 0; Mismatches 0
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Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                        298 AA;
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ZENG Z. KYAW H. FISCHER C L.

KYAW/) FISC/) LIHH/ (GENT/) MOOR/)

ZENG/

ROSEN C A.

(RUBE/)

02-FEB-2001; 12-MAR-1998; 11-SEP-1998; SOPPET D R. GENTZ R L.

WEI Y.
MOORE P A.
YOUNG P E.
GREENE J M.
FERRIE A M.

(YOUN/) (FERR/) Li Y, Zeng Z, Kyaw H, Fischer CL, Li F Wei Y, Moore PA, Young PE, Greene JM;

Rosen CA, Gentz RL,

Ruben SM, Soppet DR, Ferrie AM;

WPI; 2003-310989/30.

N-PSDB; ABX96990.

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Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; rheumatoid arthritis; diabetes mellitus; hemmatopoietic disorder; inflammatory condition; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; lschaemic brain injury; neurodegenerative disorder; atherosclerosis; blood-related disorder; thromboals; atherosclerosis; blood-related disorder; thromboals; atherosclerosis; thand disorder; hyperproliferative disorder; acute glomerulonephritis; Addison's disease; endometriosis; infectious disease; reproductive system disorder; wound repair; angiogenesis; lumphatic disorder; hair loss; body weight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein gene 25, protein.
                                                                                                                    ABU64994 standard; Protein; 298 AA
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                                                                                                                                                                                                                                        ABU64994;
                                             ABU64994
ID ABU6
RESULT 9
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Homo sapiens
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JS2002172994-A1

21-NOV-2002.

The invention relates to an isolated polypeptide comprising an amino acid sequence at least 95% identical to sequence of 28 human secreted concerts sequence at least 95% identical to sequence of 28 human secreted form, comproteins, their fragment, polypeptide domain, epitope, secreted form, variant, allelic variant, or species homologue, or the encoding concluded in ATCC 97921 and 97922. Also included are the encoding concluded in ATCC 97921 and 97922. Also included an encoding concluded acids, recombinant vectors, host cells, antibodies, and genes. The proteins and nucleic acids are useful for diagnosing, preventing, concluded in ATCC 97921 and 97922. Also included acids and genes. The proteins and nucleic acids are useful for diagnosing, preventing, prognosing or ameliorating a medical condition e.g. The proteins and nucleic acids. Severe combined immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies), accompances, severe combined immunodeficiencies, severe combined immunodeficiencies, multiple disorders, capacies, disorders, disorders, conditions (e.g. septic shock, capacies, cancers (e.g. gastric, ovarian, lung, bladder, liver and cinjury and/or stroke, traumatic brain injury), neurodegenerative complications), inflammation (e.g. hepatitis, gott, traumatic disease and Alzheimer's disease, AlbS-related disorders (e.g. parkinson's disease and Alzheimer's disease, bypass complications), inflammation (e.g. hepatitis, gott, traumatic, blood-related disorders (e.g. hepatitis, gott, traumatic, blood-related disorders, renal disorders (e.g. acute complexative disorders, renal disorders (e.g. acute complexity hyperpiliterative disorders, renal disorders (e.g. acute complexity hyperpiliterative disorders, renal disorders (e.g. acute complexity). Hyperpiliterative disorders, renal disorders (e.g. acute complexity) hyperpiliterative disorders, renal disorders (e.g. acute complexity). Hyperpiliter New human secreted polypeptides and polynucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of Claim 11; Page 186; 209pp; English. therapeutic use -

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WPI; 2003-029900/02

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SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFN 180
reproductive system disorders (e.g. endometriosis), infectious diseases, and pancreatic disorders. Many other diseases and disorders are listed in the specification. They also useful as avactine adjuvant. Further they are useful to enhance or inhibit complement mediated cell lysis, for stimulating wound and tissue repair, angiogenesis, and the repair of stimulating wound and tissue repair, angiogenesis, and the repair of pascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are represents a secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                              FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                                                                                           1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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AB271190-AB271478 represent CDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. DECTATA AB2714740 represent human secreted protein genomic fragments. The cinvention also encompasses antibodies specific for the secreted proteins, convectors and host cells comprising a nucleic acid of the invention. The secreted proteins, and recombinant convectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, coepophagus, stomach, small intestine, large intestine, large intestine, large them mouth, coepophagus, stomach, small intestine, large intestine, large intestine, large intestine, coepophagus, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the creatment of immune disorders, inflammation, infection, of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute construction, anxiets. The present sequence represents a human secreted protein of the converted protein of the converted protein of the converted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; comato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forenaic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.7%; Score 1414; DB 24;
100.0%; Pred. No. 2e-111;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                 Claim 13; Page 1046-1047; 1216pp; English
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Matches 276; Conservative
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sapiens

Homo

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, foremsics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                             115
                                                                                                                                                                                                                                                                                                                                                                                                                          83 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLGDVHVLAPAVP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                               116 SCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTG
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                                                                                                                                                                                                                                                                                                                                                     5; Gaps
                                                                                                                                                                                   Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                             Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                                                   DB 22; Length 303;
                                                                                                                                                                                                                                                                                                                                 Score 1399.5; DB 22; Length
Pred. No. 3.4e-110;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 303
                                                                                                                            , Liu C, Zhou P, Qian XB, Wang Z,
Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                              Claim 20; Page 878-879; 1275pp; English.
                                                                                                                                                                                             antibodies and research use -
                                                                     17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                  98.7%;
97.2%;
                                                              2000US-0491404
                                             25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 97.2'
Matches 273; Conservative
                                                                                                                                                        2001-476164/51
                                                                                                                                                                                                                                                                                                                  303 AA;
                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                               N-PSDB; AAH98352
          WO200154477-A2
                                                               25-JAN-2000;
                          02-AUG-2001
                                                                                                                            Tang YT,
Cao Y, Dı
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Inflammatory cell infiltration; immune response; T cell proliferation; anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy;

AAY08060 standard; Protein; 312

(first entry)

11-SEP-2000

AAY08060;

Human PRO245 protein.

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This invention describes a novel composition containing (apart from a carrier or excipient), a novel PRO245 polypeptide (1), its agonist or antagonist, or their fargements, for modulating: (i) infiltration of antagonist, or their fargements, for modulating: (i) infiltration of inflammatory cells into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects (c) [iii]. The products of the invention have anti-inflammatory.

CC in: (iii). The products of the invention have anti-inflammatory.

CC anti-autoimmune and anti-diabetic activity. (I), and its (ant) agonists anti-inflammatory are used to treat immune-related diseases.

CC particularly T cell-mediated diseases. The diseases treated include systemic upon systemic solerosis (scleroderma).

CC particularly T cell-mediated diseases. The diseases treated include stratis, spondyloarthropathics ystemic vasculitis, autoimmune compactive incommune compactive systemic vasculitis, autoimmune compactive systemic vasculitis, autoimmune compactive in autoimmune compactive in autoimmune compactive paraphic thrombocytopenia, paroxysmal nocturnal compactive and paraphic inflammatory demyelinating polymeuropathy, (idiopathic thrombocytopenia), thyroiditis, atrophic compactive hepatitis, invenile lumphersemential sclerosis, diopathic demyelinating polymeuropathy, dillain.Barre syndrome, chronic active hepatitis, primary bilary cirrhosis, granulomatous chronic active hepatitis, primary bilary cirrhosis, granulomatous contact dermatitis, and sclerosing cholangitis, inflammatory bowel disease colling: Crobin's disease), allopathic uninemented or whipple's disease, arythema multiforme, contact dermatitis, producing contact dermatitis, producing contact dermatitis, primary bilary contact dermatitis, producing contact dermatitis, primary bilary contact dermatitis, primary bilary contact dermatitis, primary bilary contact dermatitis, primary bilary contact dermatitis, antoimmune contact dermatitis, and sclerosing chorac
                                       inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis; dabetes mellitus; demyelinating polyneuropathy; Gulliain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; sthindisease; dermattis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urricaria; eosinophilic pneumonia; transplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urticaria, eosinophilic pheumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, and transplantation associated diseases (graft rejection, and graft versue-host-disease). (I), its (ant) agonists or fragment can also be used as an adjuvant in treatment of tumors. Antibodies against (I) can also be used for diagnosing such diseases. This sequence represents the human PRO245 protein described in the
cell-mediated disease; spondyloarthromathy; sclerosis; renal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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970S-0063550.
970S-0065186.
970S-0066364.
970S-0066770.
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Immune mediated thrombocytopenia, thyroiditis, Grave's disease, Hashimoto's thyroiditis, idabetes mediated invenile lymphocytic thyroiditis, atacesses. Hashimoto's thyroiditis, idabetes mediated renal disease, thyroiditis, diabetes mediated renal disease, advoided the central and peripheral nervous systems such as multiple sclerosis of the central and peripheral nervous systems such as multiple sclerosis, idopathic polyneuropathy, hepatobliary diseases, infectious hepatitis A, B, C, D, E, nonhepatotropic viruses, autoimmune chronic active enteropathy, whipple's disease, autoimmune or immune-mediated skin cholangitis, inflammatory and fibrotic lung diseases, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin diseases allergic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonias, transplantation associated diseases disease. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital microvilius arrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimen's disease; ALS, neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
       autoimmune thrombocytopenia, idiopathic thrombocytopenic purpura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration;
                                                                                                                                                                                                                                                                                                                                Score 1362; DB 20;
Pred. No. 5.3e-107;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 RKGYFSKETSFQKSNSSSKATTMSEN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 RKGYFSKETSFOKSNSSSKATTMSEN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of protein PRO245.
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                                                                                                                                                                                                                                                                                                                                96.1%;
99.2%;
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97US-0059115.
97US-0059117.
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                                                                                                                                                                                                                                                                                                                                                                       264; Conservative
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                            represents PRO245.
                                                                                                                                                                                                                                                                                                312 AA
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17-SEP-1997;
17-SEP-1997;
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                                                                                                                                                                                                      TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes A33 related antigens PRO301, PRO362 and PRO245. The methods and compositions of the invention are useful for the treatment and disquests of inflammatory disease and tumours in mammals. Such inflammatory diseases include of inflammatory bowel disease, systemic lupus erythematosis, rheumatoid arthritis, juvenile chronic systemic lupus erythematosis, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, seleratomyositis, polymyositis, idiopathic inflammatory myopathies, dermatomyositis, polymyositis, solucimmune hemolytic anemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria,
                                                                                                                                                                               FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
                                                                                                                                                                                                                                                    SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFN 180
                                                                                                                                                                                                                                                                                                                                                1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD 60
                                                                                                                                     23 YHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEWKKLGRSVSFVYYQQTLQGD 82
                                                                            Gaps
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                                        Length 312;
                                                                        Indels
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                                    Score 1362; DB 20;
Pred. No. 5.3e-107;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                 RKGYFSKETSFOKSNSSSKATTMSEN 266
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 11; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY23324 standard; Protein; 312
                                    96.1%;
99.2%;
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                                                                        Conservative
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                                                     Similarity
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Tumas D, Wood WI;
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hes 264;
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                                                                    Matches
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RESULT 13

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Length 312; Indels

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97US-0059121.
97US-0059122.
97US-0059184.
97US-0059263.
97US-0059266.
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97US-0063435.
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97US-0063870.
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97US-0065846.
97US-0065693.
97US-0066120.
97US-0066364.
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97US-0063542.
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28-0CT-1997;
29-0CT-1997;
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31-OCT-1997;
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18-NOV-1997;
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(GETH) GENENTECH INC.

Yuan J; Wood WI, Pennica D, Gurney AL, Goddard A, Chen J,

1999-229533/19. N-PSDB; AAX52225

ŏ New isolated human genes and polypeptides used in, e.g. treatment gastrointestinal ulceration

Claim 12; Fig 24; 320pp; English

AAY13344-403 represent secreted and transmembrane human proteins.
The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, as

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FKNRAEMIDENIRIKAVTRSDAGKYRCEVSAPSEQQQNLEEDTVTLEVLVAPAVPSCEVP 142
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   PRO264 can be used
                              as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirhoumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antiansemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiansemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; spetemic lupus erythematosus; rheumatodi arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; didiopathic inflammatory myopathy; sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; demyelinating disease; hepatobiliary disease; Mihipple's disease; autoimmune disease; immune-mediated skin disease; allergic disease;
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                                                                                                                                                                                                                                                                                                                96.1%; Score 1362; DB 20; Length 312; 99.2%; Pred. No. 5.3e-107; ive 0; Mismatches 2; Indels 0
for fibromodulin, e.g. for reducing dermal scarring
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99US-0123618.
99US-0123957.
99US-0125775.
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23-MAR-1999;
12-APR-1999;
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29 NOV-1999; 99WO-US28314.
30-NOV-1999; 99WO-US28313.
30-NOV-1999; 99WO-US28301.
01-DEC-1999; 99WO-US286409.
02-DEC-1999; 99WO-US286534.
02-DEC-1999; 99WO-US28665.
16-DEC-1999; 99WO-US28665.
16-DEC-1999; 99WO-US28665.
16-DEC-1999; 99WO-US3099.
30-DEC-1999; 99WO-US3099.
30-DEC-1999; 99WO-US30274.
66-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03376.
11-FEB-2000; 2000WO-US03376.
99WO-USO8615.
99US-0131445.
99US-01314287.
99US-0134287.
99WO-US12252.
99US-0141037.
99US-0145698.
                                                     99WO-US20111
99WO-US20594
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                                                                        99WO-US21090
                                                                               99WO-US21547
                                                                   99WO-US20944
20-APR-1999;
28-APR-1999;
04-MAY-1999;
02-JUN-1999;
23-JUN-1999;
26-JUL-1999;
26-JUL-1999;
                                                      01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
                                                                                     05-0CT-1999;
29-0CT-1999;
                                                                               15-SEP-1999
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(GETH) GENENTECH INC

Henzel W; Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, He Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V; Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M; Kabakoff RC, Lu Y, P. Stewart TA, Tumas D,

WPI; 2000-572271/53. N-PSDB; AAC58586.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus

Claim 33; Fig 16; 309pp; English

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, costeoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Syogren's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune con immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58379 to AAC5879 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC5842 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

312 AA; Sequence

Query Match

21; Length 312; BB Score 1362; 96.1%;

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 99.2%; Pred. No. 5.3e-107;
                  Mismatches
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Best Local Similarity
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Best Local Similarity 100.
Matches 276; Conservative
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ORGANISM: Homo sapiens
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Sequence 189, App
Sequence 131, App
Sequence 10, Appl
Sequence 23, Appl
Sequence 4, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 22, Appl
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Sequence 9, Appli
Sequence 189, App
Sequence 2, Appli
Sequence 1, Appli
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1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-188-930-189
US-09-254-465A-1
US-09-254-465A-23
US-09-254-465A-23
US-09-254-465A-24
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Maximum Match 100%
Listing first 45 summaries
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NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
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; OTHER INFORMATION: Xaa equals any of the naturally occurring
US-09-152-060-76
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Pred. No. 1.4e-130;
0; Mismatches 0;
US-08-928-383B-2
US-08-928-383B-23
US-08-928-383B-24
US-08-928-383B-26
US-09-336-536-31
US-09-336-536-42
US-09-604-107A-8
US-08-985-526-34
US-08-443-861-5
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US-07-813-593-4
US-07-977-451-6
US-07-946-507-4
US-08-252-517-6
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Patent No. 6448030
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPERENCE: PS003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
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US-08-443-861-2
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EARLIER APPLICATION NUMBER: EQ1/US98/04858

EARLIER PILING DATE: 1998-03-12

EARLIER PILING DATE: 1997-03-14

EARLIER PILING DATE: 1997-03-14

EARLIER PILING DATE: 1997-03-14

EARLIER PILING DATE: 1997-03-14

EARLIER PILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-06-05

EARLIER PILING DATE: 1997-06-05

EARLIER FILING DATE: 1997-06-05

EARLIER PILING DATE: 1997-06-05

EARLIER PILING DATE: 1997-06-05

EARLIER PILING DATE: 1997-01-05

EARLIER PILING DATE: 1997-05-05

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62 KONRAEMIDFNIRIKOVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 121
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                                                                                                                                                                                                                     APPLICANT: Strachan, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION UMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOCTUMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 30.0%; Score 426; DB 3; Length 299; Best Local Similarity 35.6%; Pred. No. 1e-33; Matches 100; Conservative 42; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 331, Application US/09188930A; Patent No. 6150502; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orner, Rene
; APPLICANT: Oncust, Rene
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000-1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
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                       US-09-188-930-189
; Sequence 189, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT

GRGANISM: Human
FEATURE:
MAME/KEY: UNSURE
MAME/KEY: UNSURE
MAME/KEY: UNSURE
LOCATION: (247)
LOCATION: (289)
US-09-188-930-189
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Mary A.
APPLICANT: Unger, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS
CURRENT APPLICATION NUMBER: US 60/05/364
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
                                                                                                   TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                              FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
                                                                                                                                                       SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
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                     23 YHKAYGFSAPKDQOVVTAVXYQBAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD 82
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                                                                                                                                                                                                                                                                                                                                           RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 9, Application US/09254465A
; Patent No. 6410708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genentech, Inc.
Ashkenazi, Avi J.
Fong, Sherman
Goddard, Audrey
Gurney, Austin L.
Napier, Mary A.
Tumas, Daniel
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; ORGANISM: Homo sapiens
US-09-254-465A-9
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US-09-254-465A-9
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: COMPOSITIONS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33 - RELATED ANTIGENS
FILE REPERENCE: Pl216R1(US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT PILING DATE: 1999-03-05
FRIOR PILING DATE: 1999-11-20
FRIOR PILING DATE: 1999-11-21
FRIOR PILING DATE: 1999-11-21
FRIOR PILING DATE: 1999-03-06
FRIOR PILING DATE: 1999-03-00
FRIOR PILING DATE: 1999-03-00
FRIOR PILING DATE: 1998-09-17
FRIOR APPLICATION NUMBER: PCT/US98/19437
                202 LSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILLGILVFGIWFAY 261
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                                                                                            241 RKGYFSKETSFQKSNSSSKA----TTMSENDFKHTKSFII 276
                                                                                                                                             : | : | : | | | : | : | | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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; Sequence 189, Application US/09312283C
; Patent No. 6573055
; GENERAL INFORMATION:
; APPLICANT: Wateson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09254465A
Patent No. 6410708
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Ashkenazi, Avi J.
Fong, Sherman
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nes 100; Conservative
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TITLE OF INVENTION: Human F11 Antigen: A Cell Surface
TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
FILE REFERENCE: GH-70150US
CURRENT PPLICATION NUMBER: US/09/462,270
CURRENT PLLING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/052,186
PRIOR FILING DATE: 1997-07-10
SNDMBR OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
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30.0%; Score 426; DB 4; Length 299;
Best Local Similarity 35.6%; Pred. No. 1e-33;
Matches 100; Conservative 42; Mismatches 99; Indels
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CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 331
LENGTH: 299
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.64
Matches 100; Conservative
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                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                  US-09-188-930-331
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KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 121
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Ashkenazi, Avi J.
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Best Local Similarity 35.9%
Matches 99; Conservative
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ORGANISM:
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; Sequence 331, Application US/09312283C
; Patent No. 657305
; GENERAL INFORMATION:
    APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Mathew
    APPLICANT: Murison, James G.
    APPLICANT: Wunble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
    TITLE OF INVENTION: and Methods for Their Use
    FILE REFERENCE: 11000.1011c2
    CURRENT FILING DATE: 1999-05-14
    NUMBER FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.0%; Score 426; DB 4; Length 299; 35.6%; Pred. No. 1e-33;
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011.2 / 09/312,283C
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 331
LENGTH: 299
                                                                                                                                                                                                                                                                               30.0%;
35.6%;
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 35.6*
Matches 100; Conservative
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Best Local Similarity 35.64
Matches 100; Conservative
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APPLICANT: Schemazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gurney, Audiey
APPLICANT: Goddard, Audiey
APPLICANT: Gurney, Audien
APPLICANT: Mary A.
APPLICANT: Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Hower of Diseases CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT PILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
142 SATIGNRAVLICSEQDGSPPSEYTWFKDGIVMPINPKSTRAFSNSSYVLNPTIGELVFDP 201
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31 YTAQSDVQVPE----NESIKLICTYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRV
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35.9%; Pred. No. 3.7e-32;
cive 49; Mismatches 116; Indels
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TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REPREBENCE: PL216R1UGS)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
FRIOR PILING DATE: 1999-11-20
FRIOR PLILING DATE: 1998-11-20
FRIOR PLILING DATE: 1997-11-21
FRIOR PLILING DATE: 1997-11-21
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-09-17
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; Patent No. 6358707
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Human F11 Antigen: A Cell Surface
; TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
; TITLE REFERENCE: GH-70150US
; CURRENT APPLICATION NUMBER: US/09/462,270
; PRIOR PILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/052,186
; PRIOR RILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.1%; Score 399; DB 4; 35.5%; Pred. No. 3.7e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 RKGYFSKETSFQKSNSSSKATTMSE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 35.5%
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AYSGFSSP
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APPLICANT: Generation:
APPLICANT: Achkenai, Avi J.
APPLICANT: Achkenai, Avi J.
APPLICANT: Achkenai, Avi J.
APPLICANT: Achkenai, Avi J.
APPLICANT: Goodard, Audrey
APPLICANT: Goodard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Uspect Mary A.
APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Wood, William I.
ITILE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
ITILE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
ITILE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR TREATED ANTIGENS
ITILE OF INVENTION: COMPOUNDS, COMPOSITIONS
ITILE OF INVENTION: DATE: 1999-03-05
CURRENT APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1999-11-21
PRIOR FILING DATE: 1999-11-21
PRIOR FILING DATE: 1999-03-10
PRIOR FILING DATE: 1999-03-10
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 23
LENGTH: 260
TWONEY TO THE TREATMENT TREATMENT
THE TREATMENT
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 30
THENDER THE TREATMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EDRVTFLPTGITFKSVTREDTGTYTCMVS--EEGGNSYGEVKVKLIVLVPPSKPTVNIPS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 VSKLDTGEYSCEARNSVGYRRCPGK-RMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AY-GFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWK-KLGRSVSFVYYQQTLQGDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.1%; Score 399; DB 4; Length 260; Best Local Similarity 35.5%; Pred. No. 3.6e-31; Matches 94; Conservative 39; Mismatches 96; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|:|: | : |:|:
239 SRGHFDR----TKKGTSSKKVIYSQ 259
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                                                                                                                                            Sequence 23, Application US/09254465A Patent No. 6410708
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09254465A
Patent No. 6410708
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney, Austin L.
Napier, Mary A.
Tumas, Daniel
Wood, William I.
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Ashkenazi, Avi J.
Fong, Sherman
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
US-09-254-465A-23
                                                                                                           US-09-254-465A-23
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APPLICANT: APPLICANT:

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APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Goddard, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Nood, Milliam I.
APPLICANT: Wood, Milliam I.
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFERENCE: P1216R1(US)
FILE REFERENCE: 1999-03-05
FILE REFERENCE: 1999-03-05
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-03-05
FRIOR FILING DATE: 1998-09-17
FRIOR FILING DATE: 1998-09-17
FRIOR FILING DATE: 1998-03-05
                                    84 EDRVIFLPTGITFKSVTREDIGIYICAVS--EEGGNSYGEVKVKLIVLVPPSKPTVNIPS 141
                                                                                                                                             62 KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 121
                                                                                                            122 SALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 GELYKNRYSISNNAEQSDASITIDQLTWADNGTYECSVSLMSD----LEGNTKSRVRLLV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 LVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSY 168
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16.3%; Score 231; DB 4; Length 270;
Best Local Similarity 28.6%; Pred. No. 1.1e-14;
Matches 72; Conservative 41; Mismatches 97; Indels
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US-09-254-465A-24
Sequence 24, Application US/09254465A
Patent No. 6410708
GENERAL INFORMATION:
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234 ALIIIGIIIYCC 245
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-254-465A-24
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US-09-254-465A-26
Sequence 26, Application US/09254465A
Patent No. 6410708
GENERAL INFORMATION:

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APPLICANT: Genentech, Inc.

APPLICANT: Ablkenazi, Avi J.

APPLICANT: Ablkenazi, Avi J.

APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Tunes, Daniel

APPLICANT: Wapier, Mary A.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

TILLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT

TILLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT

TILLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS

FILE REFERENCE: P1116 DATE: 1999-03-05

CURRENT PILING DATE: 1999-11-20

PRIOR FILING DATE: 1999-11-21

PRIOR FILING DATE: 1999-03-10

PRIOR FILING DATE: 1999-03-17

PRIOR FILING DATE: 1999-03-17

SEQ ID NO 26

LENGTH: 273

TWORT: DATE

TWORT: DATE

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Patent No. 5712369

GENERAL INFORMATION:
APPLICANT: Simpson, Richard J.; Welt, Sydney; Ritter, Gerd;
APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
APPLICANT: Statinel, B.; J.; Hong; Burgess, Anthony W.;
APPLICANT: Getinel, B.; J.; Hong; Burgess, Anthony W.;
APPLICANT: Good Cell and Colon Cancer Cell
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 GD-FKNR-----AEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDT---VTLEV 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 SVETPQDVLRASQGKSVTLPC-TYHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKNYIH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 SAPKDQQVVTAVXYQEAILACKTPKKTVXSR---LEWKKL----GRSVSFVYYQQT-LQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.3%; Score 231; DB 4; Length 273; 28.6%; Pred. No. 1.1e-14; tive 41; Mismatches 97; Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.3%
Best Local Similarity 28.6%
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 AVVVVALVISVC 232
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US-09-254-465A-26
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Query Match 16.3%; Score 231; DB 1; Length 319;
Best Local Similarity 28.6%; Pred. No. 1.4e-14;
Matches 72; Conservative 41; Mismatches 97; Indels 42; Gaps 11;
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,495B
FILING DATE: 0.2-Feb-1996
FILING DATE: 0.4-Aug-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 0.9/511,876
FILING DATE: 0.4-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: HAMBOR: NO. 5712569man D.
REGISTRATION NUMBER: 10,946
FILING TOWNEY STATION NUMBER: 10,946
FILING TOWNEY STATION INFORMATION:
TELECOMMUNICATION INFOR
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Search completed: December 9, 2003, 17:14:23 Job time : 14.4251 secs

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December 9, 2003, 17:13:07 ; Search time 25.4843 Seconds (without alignments) 2014.238 Million cell updates/sec
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1418
1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-799-777-30
US-10-139-849-2
US-10-192-791-2
US-09-853-161-76
US-09-853-161-76
US-09-852-797-76
US-09-909-320-64
US-09-909-320-64
US-09-909-320-64
US-09-905-391A-64
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Perfect score:
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9000	ALIGNMENTS 63 R. isa A. stribute, 11 ck Drive 13 stribute, 12 ck Drive 10 00 11 11 12 13 13 13 13 13 13 13 14 15 16 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18
-60-Sn -6	AI 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
######################################	IS/097457 Kenneth John M. Rese, L. Bayie Bayie SECRETE SECRETE ENCOINN SECRETE ENCOINN SECRETE ENCOINN SERS SECRETE SERS SECRETE SERS SECRETE SERS SECRETE SERS SECRETE SERS SERS SERS SERS SERS SERS SERS
	3-38 8, Application US/09745763 US20020065394A1 UNFORMATION: LINFORMATION: Lavalitie, Edward R. Lavalitie, Edward R. Lavalitie, Edward R. Colling-Racie, Lisa A. Evans, Cheryl Merberg, David Treacy, Maurice Spaulding, Vikki LE OF INVENTION: SECRETED PROTEINS ENCODING THEM STREET: 87 CambridgePark Drive STREET: 84 CAMBRE: 18-000 SOFTWARE: Patentin Release #1.0, REMT APPLICATION NUMBER: 1333 ECCMMUNICATION INFORMATION: TELEFPAX: (617) 898-8284 TELEFPAX: (617) 898-8284
	icat Jaco Jaco McC Jaco Jaco Jaco SEQU SEQU SEQU SEQU A TXI TINE: SPT TXI SPT
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Application Si210020065394 Si220020065394 FPORMATION CONT. Lavall COllin Evans, Merber Yeavall Spauld OF INVENTIO SPONDENCE AD SPANTION STREET: 87 C CTIT: Cambri CTIT: Cambri STREET: 87 C CTIT: Cambri STREET: 87 C COUNTRY: U.S STREET: PAI MEDIUM TYPE:
1362 1362 1362 1362 1362 1362 1362 1362	SEQUENCE 38, Application US/097457 Batent No. US2002065394A1 GENERAL INFORMATION: LAVAIII, EAWARGE LAVAIII, EAWARGE LAVAIII, EAWARGE LAVAIII, EAWARGE LAVAIII, EAWARGE COLIINB-RACIE, DAVID TITLE OF INVENTION: SECRETE Spaulding, Vikki TITLE OF INVENTION: SECRETE NUMBER OF SEQUENCES: 219 CORRESPONDENCE ADDRESS: ADDRESSES: GENERICS TITLE OF INVENTION: SECRETE NUMBER OF SEQUENCES: 219 CORRESPONDENCE ADDRESS: ADDRESSES: GENERICS TITLE OF INVENTION SECRETE OUNTRY: U.S.A. ZIRET: 87 CambridgePa CITY: CambridgePa CONPUTER: INB PC COMPA CONPUTER: INB PC COMPA COMPUTER: INB PC COMPA COMPUTER: INB PC COMPA COMPUTER: INB PC COMPA COMPANIES PATONIN PROMATION: NAME: SPETICATION NUMBER: 18 REGISTRATION NUMBER: 18 REGISTRATION NUMBER: 18 REGISTRATION NUMBER: 18 TELEFPHONE: (617) 876-585
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61 FKWRAEMIDFNIRIKWVTRSDAGKYRCEVSAPSEOGONLEEDTVTLEVLVAPAVPSCEVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMVTKTGTLQFN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                    23 YHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEWKKLGRSVSFVYYQQTLQCD
                                                                                                                                                                                                                                                                                                                                                                                                      1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
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Barros, Maria Pia
TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN
JUNCTIONAL ADHESION PROTEIN (JAM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
Suite 4700
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/139,849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                               Score 1415; DB 9;
Pred. No. 2.5e-125;
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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APPLICATION NUMBER: US/09/643,929
FILING DATE: 23-Aug-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
                  TELEPAX: (650) 845-4166
INFORMATION FOR ESQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acida
TYPE: amino acida
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: DUODNOTO2
CLONE: 1704050
(650) 855-0555
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CLASSIFICATION: <Unknown>
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Publication No. US20030079238A1
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Best Local Similarity 99.3
Matches 274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: IL
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     US-09-799-777-30
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US-10-139-849-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
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                                                                                                                                                                                                                                                                                                          1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                   Gaps
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Corley, Neil C.
Guegler, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
CORRESPONDENCE: 154
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                       Length 298
                                                                                                                                                                                                                                                                Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                Query Match 99.8%; Score 1415; DB 9; Best Local Similarity 99.3%; Pred. No. 2.5e-125; Matches 274; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/002,485
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION WHBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
                                                                                       ; TOPOLOGY: linear; SEQUENCE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 38: US-09-745-763-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/09799777
Patent No. US20020091244A1
GENERAL INFORMATION:
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                                       LENGTH: 298 amino acida
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
INFORMATION FOR SEQ ID NO: 38
                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-799-777-30
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LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-853-161-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
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                                                                 263 RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                           Sequence 76, Application US/09853161

Batent No. US2002007655A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TILLE REFERENCE: PZ003P3

CURRENT APPLICATION NUMBER: US/09/853,161

CURRENT PILING DATE: 2001-05-11

PRIOR PLING DATE: 1998-09-11

PRIOR PLING DATE: 1998-09-11

PRIOR PLING DATE: 1998-09-11

PRIOR PLING DATE: 1998-03-12

PRIOR PLING DATE: 1998-03-12

PRIOR PLING DATE: 1997-03-14

PRIOR PLING DATE: 1997-05-30

PRIOR PLING DATE: 1997-05-30
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
                                                                                                                                                                                                           US-09-853-161-76
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Publication No. US20030130166A1
GENERAL INFORMATION
TITLE OF INVENTION: A Polynuclectide Encoding a Human Junctional Adhesion Protein (CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                         Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                  Query Match 99.8%; Score 1415; DB 15; Best Local Similarity 99.3%; Pred. No. 2.5e-125; Matches 274; Conservative 0; Mismatches 2;
                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                  INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TELEPHONE: 312-616-5400
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Best Local Similarity 99.31
Matches 274; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 298
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TYPE: PRT
ORGANISM: Homo Bapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (42)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (58)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (58)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-797-76
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                                                                                                                                                                                263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                            241 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                           Sequence 76, Application US/09852797
Patent No. US20020172994A1
GENERAL INFORMATION:
APPLICANT: Roser at al.
TITLE OP INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PZOO19P2
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR PELICATION NUMBER: 60/265,583
PRIOR PELICATION NUMBER: 09/152.060
PRIOR PELICATION NUMBER: 09/152.060
PRIOR PELING DATE: 1998-09-11
PRIOR PELING DATE: 1998-09-11
PRIOR PELING DATE: 1997-03-12
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-06-06
PRIOR PEL
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (58); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-852-659A-76
   203 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKNRAEMIDFNIRIKONVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
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                                                                                                        263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 28 Human Secreted Proteins
FITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-14
PRIOR PELLING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR PELLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR APPLICATION NUMBER: 60/048,135
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR PELLING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR PELLING DATE: 1997-06-06
PRIOR PELLING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
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Sequence 76, Application US/09852659A

; Patent No. US20020077287A1

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
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82

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203 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 262
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timethy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-11
CURRENT APPLICATION UNDER: US/09/909,088B
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Pred. No. 2.7e-120;
0; Mismatches 2;
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR PPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
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Patent NO. US20020146709A1
GRENAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botsein, David
APPLICANT: Botsein, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Glang
Gerber, Hanspeter
Gerritsen, Mary E.
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Best Local Similarity 99.2%;
Matches 264; Conservative
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Hillan, Kenneth, J.
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Mather, Jennie P.
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US-09-909-320-64
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 60/143,048
PRIOR PLILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-30
PRIOR PELLING DATE: 1999-11-30
                                                        203 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 262
                       TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                                                                                                    263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                     241 RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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; Patent No. US20020132240A1
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-909-320-64
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APPLICANT:
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99.2%; Pred. No. 2.7e-120;
ive 0; Mismatches 2;
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane F
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT APPLICATION NUMBER: US/0143,048
PRIOR PLILING DATE: 2001-07-12
PRIOR PLLING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-09-18
PRIOR PLLING DATE: 1999-09-18
PRIOR PLLING DATE: 1999-09-18
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-20
PRIOR PLLING DATE: 1999-12-02
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Best Local Similarity 99.2
Matches 264; Conservative
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                                 PRIOR APPLICATION NUMBER: 105 (0/145, 048)
PRIOR APPLICATION NUMBER: US 60/145, 048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PEL
OR APPLICATION NUMBER: PCT/USO0/04414

OR FILING DATE: 2000-02-22

OR APPLICATION NUMBER: US 60/143,048

OR PILING DATE: 1999-07-07

OR APPLICATION NUMBER: US 60/145,698

OR PILING DATE: 1999-07-28

OR PILING DATE: 1999-07-28

OR PILING DATE: 1999-07-28

OR PILING DATE: 1999-07-28

OR APPLICATION NUMBER: PCT/US99/20594

OR PILING DATE: 1999-09-08

OR PILING DATE: 1999-09-13

OR APPLICATION NUMBER: PCT/US99/21090

OR PILING DATE: 1999-09-15

OR APPLICATION NUMBER: PCT/US99/21090

OR PILING DATE: 1999-09-15

OR APPLICATION NUMBER: PCT/US99/23089

OR PILING DATE: 1999-10-05

OR PILING DATE: 1999-11-29

OR APPLICATION NUMBER: PCT/US99/2813

OR PILING DATE: 1999-11-29

OR APPLICATION NUMBER: PCT/US99/2813

OR PILING DATE: 1999-11-29

OR APPLICATION NUMBER: PCT/US99/2813

OR PILING DATE: 1999-11-29

OR APPLICATION NUMBER: PCT/US99/28564

OR PILING DATE: 1999-11-29

OR APPLICATION NUMBER: PCT/US99/28565

OR APPLICATION NUMBER: PCT/US99/28565
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Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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Matches 264; Conservative
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SEQ ID NO 64
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ORGANISM: Homo sapiens
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US-09-905-291A-64
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203 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVGLGVCYAQ 262
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/902,853

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US/09/665,350

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-13

PRIOR PRIOR DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/2854

PRIOR PLING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR PLING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR PLING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR APPLICATION NUMBER: PCT/US99/28056

PRIOR PLING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28091

PRIOR PLING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28091

PRIOR APPLICATION NUMBER: PCT/US99/28091
                                                            241 RKGYFSKETSFOKSNSSSKATTMSEN 266
                                                                                              263 RKGYFSKETSFOKSNSSSKATTMSEN 288
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                          Sequence 64, Application US/09902853
Publication No. US20020192659A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                             APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                  Sherman
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APPLICANT:
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Pred. No. 2.7e-120;
0; Mismatches 2; Indels 0;
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99.2%;
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Best Local Similarity 99.2°
Matches 264; Conservative
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ORGANISM: Homo sapiens
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PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PELING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-09
PRIOR PLING DATE: 1999-09-09
PRIOR PELING DATE: 1999-09-09-09
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
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PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
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                                 PILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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Best Local Similarity 99.2%; Pred. No. 2.7e-120;
Matches 264; Conservative 0; Mismatches 2;
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
SEQ ID NO 5: 423
LENGTH: 312
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Publication No. US20020197671A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-dlage
Gerber, Hanapeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William, I.
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Botstein, David
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Eaton, Dan L.
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                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo Sapien
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Paoni, Nicl
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                                                                                                                                                                                                                                                                                                                                                                           TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                                                                                                                 23 YHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEWKKLGRSVSFVYYQQTLQGD 82
                                                                                                                                                                                                                                                                                                                                                                                                      1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                          Gaps
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                                                               Length 312;
                                                                                                      Indels
                                                             96.1%; Score 1362; DB 10; 99.2%; Pred. No. 2.7e-120; ive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKGYFSKETSFQKSNSSSKATTMSEN 288
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US-09-907-841-64

i Sequence 64, Application US/09907841
i Publication No. US20020198366A1
i GENERAL INFORMATION:
i APPLICANT: Genentech, Inc.
i APPLICANT: Ashkenazi, Avi
                                                       Query Match
Best Local Similarity 99.2
Matches 264; Conservative
; ORGANISM: Homo Sapien
US-09-907-824-64
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203 TVSKLDTGEYSCEARNSVGYRRCPGKRAQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 262
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,011

CURRENT FILING DATE: 2001-07-11

PRIOR PELICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR PLING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PELING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-8

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21547
OR FILING DATE: 1999-09-15
OR FILING DATE: 1999-10-15
OR FILING DATE: 1999-10-05
OR FILING DATE: 1999-11-29
OR APPLICATION NUMBER: PCT/US99/28214
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: 1999-11-29
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: 1999-11-39
                                                                                                          263 RKGYFSKETSFOKSNSSSKATTMSEN 288
                                                                                241 RKGYFSKETSFQKSNSSSKATTMSEN 266
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J.
Grimaldi, Christopher J.
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Publication No. US20030003530A1
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFREENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,841

CURRENT PILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PRIOR PRIOR DATE: 1999-07-28

PRIOR PRIOR PRIOR DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PRIOR PRIOR DATE: 1999-09-15

PRIOR PRIOR PRILING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PRIOR PLING DATE: 1999-11-29

PRIOR PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                     Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                          Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Williams, P. Mickey
Wood, William, I.
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Gerritsen, Mary E.
                             Desnoyers, Luc
Saton, Dan L.
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Matches 264; Conservative
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; ORGANISM: Homo sapiens
US-09-907-841-64
                                                                                                                                                                                                                                Goddard, A.
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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96.1%; Score 1362; DB 11; Length 312;
Best Local Similarity 99.2%; Pred. No. 2.7e-120;
Matches 264; Conservative 0; Mismatches 2; Indels 0
## PRIOR APPLICATION NUMBER: PCT/US99/30911
| PRIOR FILING DATE: 1999-12-20 |
| PRIOR PILING DATE: 1999-12-20 |
| PRIOR FILING DATE: 1999-12-20 |
| PRIOR FILING DATE: 1999-12-20 |
| PRIOR PLICATION NUMBER: PCT/US00/00219 |
| PRIOR PILING DATE: 2000-01-05 |
| NUMBER OF SEQ ID NOS: 423 |
| SEQ ID NO 64 |
| LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-64
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Search completed: December 9, 2003, 17:22:01 Job time : 25.4843 secs

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                  Copyright
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protein - protein search, using sw model ĕ

December Run on:

9, 2003, 17:09:51; Search time 13.9443 Seconds (without alignments) 1903.477 Million cell updates/sec

US-09-852-797-76_COPY_23_298 1418 1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276 Title: Perfect

score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description	junctional adhesio		II.	fasciclin II PI-li	C-89	titin - h	Bine	nonspecific cross-			$\overline{}$		ਕ	ErbB kinase activa	U	hypothetical prote		ъ	cell adhesion prot	neural cell adhesi	protein-tyrosine-p	protein-tyrosine-n	biliary glycoprofe	Drotein-tvrogine-n	Drotein-tvrogine-n	PCTO-ATDASP Drecir		ן פר בר	cell
SUMMARIES	OI	S56749	JC7780	A41054	B41054	T29757	138346	A41228	A27681	JC5702	JC5701	T23007	T34416	JE0100	JC5700	JC1508	T46283	T20992	T43290	S19247	JN0635	158148	S46217	S34338	150212	550893	A44783	JE0099	IJXLNL	T30532
	88	;						7										~			Н	~	0	~	N	~	~	~	-	7
	Query Match Length	299	365	811	873	6642	7962	1367	344	860	868	1328	2783	725	820	521	773	5175	5198	1033	1092	1501	1863	521	1499	1907	519	725	1088	1277
d	Query	30.0	13.4	13.1	13.1	12.1	11.5	11.3	11.1	11.1	11.1	11.0	11.0	10.9	10.9	10.8	10.7	10.7	10.7	10.7	10.6	10.6	10.6	10.6	10.6	10.6	10.5	10.4	10.4	10.4
	Score	426	190.5	186	186	171	163.5	160.5	157	157		155.5	S	155	155	153.5	152	152		151.5	151	151		150.5	150	150	148.5	148	148	148
	Result No.	1	8	m	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53

neural cell adhesi	connectin/titin -	biliary glycoprote	transmembrane carc	biliary glycoprote	leukocyte antigen-	biliary glycoprote	neural cell adhesi	kinase-like protei	amalgam protein pr	carcinoembryonica	hypothetical prote	hypothetical prote	8ax-3 protein - Ca	neuroalian - fruit	perlecan precursor
IJCHNL	T42633	JH0394	C30127	A32164	TDHULK	WMMSR1	IJHUNG	A39712	A31923	A34815	T33433	T29549	T42405	A32579	A38096
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ALIGNMENTS

C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C.Accession: A59406; S56749

CiAccession: A59406; S56749

Riozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; i J. Immunol. 163, 535-557, 1999

Riozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; i J. Immunol. 163, 535-557, 1999

A.Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut: A;Reference number: A59406; MUID:99323940; PMID:10395639

A.Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut: A;Reference number: A59406; MUID:95326797; PIDN:AAD42050.1

R.;Residues: 1-299 < CZA.
A;Residues: 1-299 < CZA.
A;Residues: S56749

A;Reference number: S56749; MUID:95374438; PMID:7646439

A;Reference number: S56749

A;Reference number: S56749

A;Reference number: S56749

A;Residues: 28-49, X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLAXY;'LT',206,'X'
A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLAXY;'LT',206,'X'
A;Note: the order of the peptides other than the amino terminus was not determined CGenetics:
CGenetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane F;26-299/Product: junctional adhesion molecule #status predicted <AMAT>

7; 99; Indels 40; Gaps Query Match
30.0%; Score 426; DB 2; Length 299;
Best Local Similarity 35.6%; Pred. No. 1.4e-26;
Matches 100; Conservative 42; Mismatches 99; Indels 4

62 KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 121 84 EDRVTFLPTGITFKSVTREDIGIYTCMVS--EEGGNSYGEVKVKLIVLVPPSKPTVNIPS 141 SALSGTWVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFNT 181 VSKLDTGEYSCEARNSVGYRRCPGK-RMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240 61 83 4 AY-GFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWK-KLGRSVSFVYYQQTLQGDF 122 g 셤 ઠ ઠે ਠੇ g õ

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241 RKGYFSKETSFOKSNSSSKA----TTMSENDFKHTKSFII 276 <u>:</u> = = =

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fasciciin II PI-linked splice form precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C;Accession: B41054
R;Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
R;Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
A;Title: Gnetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A;Title: analysis of growth cone guidance in Drosophila: fasciclin II functions
A;Accession: B41054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: FlyBase:Fas2
A,Cross-references: FlyBase:FBgn0000635
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C;Keywords: transmembrane protein
                                                               KORRAEMIDFNIRIKOVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 121
                                                                                                                                                                                                                                                  122 SALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNT 181
                                                                                                                                                                                                                                                                                                         291
                                                                                                                                                                                                                                                                                                                                                                VSKLDTGEYSCEARNSVGYRRCPGK-----RMQVDDL-NISGIIAAVVVVALVISVCGLG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 KNRAEMIDFNIRIKANTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 SALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 VSKLDTGEYSCEARNSVGYRRCPGK-----RMQVDDL-NISGIIAAVVVVALVISVCGLG 235
                                                                                                                                                                          240 EAVEGKPFAANCTAR-GKPVPEISWIRDATQL------NVATADRFQVNPQTGLVTISS
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
                               SAPKDQQVVTAVXYQEAILACKT---PKKTVXSRLEWKKLG---RSVSFVYYQQTLQGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 SAPKDQQVVTAVXYQEAILACKT---PKKTVXSRLEWKKLG---RSVSFVYYQQTLQGDF
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
13.1%; Score 186; DB 2; Length 87
Best Local Similarity 24.6%; Pred. No. 6.7e-07;
Matches 67; Conservative 50; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 VCYAQRKGYFSKETSFQKSNSSSKATTMSEND 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 TCRA--KGRPAPAITFRRWGTQEEYTNGQQDD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | : | : | : | TCRA--KGRPAPAITFRRWGTQEEYTNGQQDD 371
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-873 <GRE>
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                                                                                                                      Coxsackie- and adenovirus receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Sate: 02-Apr-2002 #sequence_revision 02-Apr-2002
R;Thoelen, I:; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptc
A;Teterence number: JC7780
A;Reference number: JC7780
A;Accession: JC7780
A;Molecule type: mRNA
A;Residues: 1-365 <THO>
A;Residues: 1-365 <THO>
A;Cross-references: GB:AY033651
C;Comment: This protein serves as the primary adenoviral attachment site on bovine cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 21.Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C;Accession: A41054
R;Grenningloh, G; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A;Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions A;Reference number: A41054; MUID:92005695; PMID:1913818
A;Accession: A41054
A;Accession: A41054
A;Retain preliminary
A;Molecule type: mRNA
A;Residues: 1-811 cGRE>
A;Cross_references: GB:M77165; NID:g157402; PID:g157403
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A,Cross-references: Flybase:FBgn0000635
C,Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C,Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fasciclin II, transmembrane splice form precursor - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 GSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRC------PGKRMQVD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 DSOKLPTSWLPEMTSPVISVKNASAEYSGTYTCTVRNRVGSDOCLLRLDVVPPSNRAGTI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 DLNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQ-----KSNSSSKATTM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 AGAVIGTLLALVLIALIVFCCH----KKRREEKYEKEVHHDIREDVPPPKSRTSTARSYI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLSITTPEOMIEKAKGETAYLPCKFTLGPEDQGPLDIEWLLSPADNQKVDQVIILYSGDK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 VSFVYYQQTLQGDFKNRAEMI------DFNIRIKNVTRSDAGKYRCEV-SAPSEQGQNL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i34 Q-----LTVLVKPSGIRCYVDGSEEIGNDFKLKCEPKEGSLPLRYEWQK-----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GFSAPKDQQVVTAVXYQEAILACK---TPKKTVXSRLEW-----KKL-----GRS
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Local Similarity 24.6%; Pred. No. 6.2e-07;
es 67; Conservative 50; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
SRGHFDRT----KKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 190.5; DB 2; 24.1%; Pred. No. 1e-07; ive 43; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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2817 KAENSIG 2823
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A; Status: preliminary
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                            A;Map position: 1
A;Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1;
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rilabeit, S.; Kolmerer, B. Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3930 PDFLQPVKPAVVTVGETAVLEGKI-----SGKPKPSVKWYKNGBELKPSDRVKIE-- 3979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3823 GRGAPBFVELLRSCTVTEKQQAILKCKV-KGEPRPKIKWTKEGKEVEM------SAR 3872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2666 KSIILESTYTGTLPISVTWKKDGFNITTSEKCNIVTTEKTC------ILEILN 2712
C;Accession: T29757

R;Du, Z.; Le, T.T.; Wilson, R.

Bubmitted to the EMBL Data Library, May 1997

A;Description: The sequence of C. elegans cosmid C09D1.

A;Reference number: Z20679

A;Accession: T29757

A;Accession: T29757

A;Residues: pre-liminary; translated from GB/EMBL/DDBJ

A;Residues: 1-6642 cDUZ>

A;Residues: 1-6642 cDUZ>

A;Residues: 1-6642 cDUZ>

A;Experimental source: strain Bristol N2; clone C09D1

C;Genetics: CESP:unc-89

A;Genetics: CESP:unc-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRAEMID----FNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 P-----SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 VTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEV----PSSALSGTVVELR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 CQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GFSAPKDQQVV---TAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: 138346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-7962 <RES>
A;Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (mān)
C;Date: 29-May 1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 171; DB 2; Length 6642; 28.1%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31
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138346
elastic titin - human (fragment)
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Best Local Similarity
Matches 53; Conserv
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Best Local S
Matches 61
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protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recepi C;Species: Mus musculus (house mouse)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 04-Feb-2000
C;Accession: A41228; A46065; T58365; S18832; S29991
R;Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R. Aproc. Natl. Acad. Sci. US.S. 88, 9026-9030, 1991
A;Title: A receptor tyrosine kinase CDNA isolated from a population of enriched primitinal, Raference number: A41228; MUID:92020984; PMID:1717995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1367 (MAT>
A;Residues: 1-1367 (MAT>
A;Cross-references: GB:X559397; NID:g50976; PIDN:CAA42040.1; PID:g50977
B;Millauer. B.; Wizigmann-Voos, S.; Schnurch, H.; Martinez, R.; Moller, N.P.; Risau, W. Cell 72, 835-846, 1993
A;Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a major A;Reference number: A46065; MUID:93208880; PMID:7681362
A;Accession: A46065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1.24, "T', 26-782, 'VL', 785-916, 'C', 918-1367 <MIL>
A; Residues: 1.24, "T', 26-782, 'VL', 785-916, 'C', 918-1367 <MIL>
A; Cross-references: GB: X70842; NID: 957923; PIDN: CAA50192.1; PID: 957924
A; Note: submitted to the EMBL Data Library, January 1993
A; Note: sequence extracted from NCBI backbone (NCBIP: 128064)
B; Note: Reid, H.H.; Bernard, O.; Ziemiecki, A.; Wilks, A.F.
Oncogene 8, 11-18, 1993
A; Title: NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from B10 of A; Reference number: 158365; MUID: 93141255; PMID: 8423988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EVSAPSEQGQNLEEDTVTLEV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 622 ILIVAFONASLODOGDYVCSAODKKTKKRHCLVKQLIILERMAPMITG-NLENOTTII-- 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   679 ------GETIEVTC-PASGNPTPHITWFKDNETLVEDSGIVLRDGNRNL 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-678,'D',680-1340,'RSPPV' <OEL>
A;Cross-references: GB:S53103; NID:g264004; PIDN:AAB25043.1; PID:g264005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 QEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFN----
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Best Local Similarity 24.8%; Pred. No. 0.00012;
Matches 53; Conservative 23; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonspecific cross-reacting antigen precursor - human N;Alternate names: NCA; TEX/NCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-678,'D',680-1340,'RSPPV' <0EL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 ---IRIKNVTRSDAGKYRC------
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embry

us-09-852-797-76_copy

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A,Map position: 19913.2-19913.2
A;Introns: 22/1
C;Superfamily: carcinoembryonic antigen; carcinoembryonic migen; carcinoembryonic antigen; carcinoembryonic antigen; precursor amino-terminal homology cCEAN>F;1-134/Domain: signal sequence #status predicted cSIG>F;35-320/Product: nonspecific cross-reacting antigen #status experimental cMAT>F;160-217/Domain: immunoglobulin homology cIMM1>F;252-301/Domain: immunoglobulin homology cIMM1>F;252-301/Domain: immunoglobulin homology cIMM1>F;252-301/Domain: immunoglobulin homology cIMM2>F;252-301/Domain: immunoglobulin homology cIMM2
                                                                                                                                                              AjStatus: preliminary; not compared with conceptual translation
Modecule type: DNA
AjResidues: 35-137,11,139-141 «KH2»
CjComment: This protein appears to be processed at the carboxyl terminus and anchored tl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;104,111,15,152,173,197,224,756,274,288,292/Binding site: carbohydrate (Asn) (covalen F;309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;309/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature for
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A.fitle: A novel brain-derived member of the epidermal growth factor family that intera. A. Reference number: JC5700; MUID:98006324; PMID:9348101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Comment: This protein is a member of the epidermal growth factor family. It is functi-
thing the differentiation of MDA-MB-453 cells.
C;Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; immun
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           θ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TFQQSTQELFIPNITVNN 293
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A;Experimental source: PC-12 cell
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,Residues: 1-860 <HIG>
,Cross-references: DDBJ:DB9996; NID:g2605631; PIDN:BAA23345.1; PID:g2605632
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
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F;274-327/Domain: EGF homology <EGF>
F;361-397/Domain: EGF homology <EGF>
F;422-444/Domain: hydrophobic #status predicted <HYD>
F;163,294,467/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:120221; OMIM:163980
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A; Status: nucleic acid sequence not shown
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A;Molecule type: mRNA
A;Residues: 'F',212-213,223-860 <HI2>
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48; Conserv
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Best Local S
Matches 48
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31 Mar:1999 Hesquence revision 16-Sep-1992 #text change 31-Jan-2000
C;Accession: AS6902; A29975; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R;Oikawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biochem. Biophys. Res. Commun. 146', 464-469, 1987
A;Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene A;Reference number: A26902; MUD:87298464; PMID:3619891
A;Accession: A26902
A;Molecular type: DNA
A;Residues: 1-141 <oli>A;Atle: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami A;Reference number: A29875; MUD:87298464; PMID:303072
A;Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami A;Reference number: A29875; MUD:87204248; PMID:3033672
A;Title: Molecular Cloning of a gene belonging to the carcinoembryonic antigen gene fami A;Reference number: A29875; MUD:87204248; PMID:3033672
A;Molecule type: DNA
A;Rosidues: 23-141 < THO>
A;Toss-references: GB:ML6337
A;Note: the authors translated the codon ACT for residue 64 as Tyr
B;Tawarsay: Y; Oikbawa, S; Matsuoka, Y; Kosaki, G; Nakazato, H.
B;Oohem: Biophys. Res Commun. 150, 89-96, 1998
A;Title: Primary structure of nonspecific crossreacting antigen (NCA), a member of carcin A;Residues: 1-738 /V, 24681
A;Rosidues: 1-738 /V, 24681
A;Rosidues: 1-738 /V, 24681
A;Residues: 1-738 /V, 24681
A;Residues: 3-59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and CA;Reference number: A21037; MUD:89122014; PMID:3220478
A;Reference number: A21037; MUD:99122014; PMID:3220478
A;Reference number: A21037; MUD:99122014; PMID:3220478
A;Reference number: A21037; MUD:99122014; PMID:3220478
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A; Molecule type: mRNA
A; Redecule type: mRNA
A; Redecule type: mRNA
A; Redecule type: mRNA
A; Coss - references: GB M29541; NID: g189103; PIDN: AAA59915.1; PID: g189104
A; Cross - references: GB M29541; NID: g189103; PIDN: AAA59915.1; PID: g189104
A; Note: the authors translated the codon TTG for residue 138 as Phe
A; Note: the authors translated the codon TTG for residue 138 as Phe
A; Note: the authors translated the codon TTG for residue 138 as Phe
A; Note: the authors an example of the codon TTG for residue 138 as Phe
A; Note: the authors translated the codon TTG for residue 138 as Phe
A; Note: the authors and the codon TTG for residue 138 as Phe
A; Note: the authors are not codon TTG for the nonspecific cross-reacting antigen (NCA; Reference number: A29918; MUID: 88139389; PMID: 2830274
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Moser. G; Pande, H; Lee, T.D.; Shively, J.E.
B; Paxton, R.J.; Moser. G; Pande, H; Lee, T.D.; Shively, J.E.
Broc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A; Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A; Reference number: A26414; MUD: 87147209; PMID: 3469650
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: Drotein
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A;Accession: A27709
A;Molecule type: protein
A;Rosidues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-235
R;Hefta, S.A.; Paxton, R.J.; Shively, J.E.
B;Hefta, S.A.; Paxton, R.J.; Shively, J.E.
A;Hefta, S.A.; Paxton, R.J.; Shively, J.E.
A;Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and ind
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A; Residues: 1.344 cNEUD-
A; Cross-references: GNEM18216; GB:J03550; NID:g178690; PIDN:AAA51739.1; PID:g178691
A; Cross-references: GNEM18216; GB:J03550; NID:g178690; PIDN:AAA51739.1; PID:g178691
R; Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biochem. Biophys. Res. Commun. 133, 1105-1115, 1988
A; Fitle: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and
A; Reference number: A27709; MUID:88268882; PMID:3390172
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11.1%; Score 157; DB 2; Length 860;

Query Match

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A;Map position: X
A;Introns: 34/1; 85/3; 133/3; 182/2; 220/3; 262/2; 390/3; 442/2; 493/3; 563/2; 586/3; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 5
A;Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 2!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 TITWLFEKÇKLTESRKHKLTKNGSVLKIFPFLNTDIGQYECVASNGEESKSHI--FSVSL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2666 VQTCEKNRAELRASF-----SGTPAPACRWFYNGNELIDGLDGYTITSSDINSS--- 2714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2715 -----LINSVDKKHFGEYLCTIRNQNGEELANAMILSEGEC-RKHPRIDIVFVCNSF1 2767
                             A.Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1328 «MIL>
A;Residues: 1-1328 «MIL>
A;Cross-references: EMBL:Z68005; PIDN:CAA91994.1; GSPDB:GN00028; CESP:K09C8.5
A;Experimental source: clone F59F3
B;Kershaw, J.
Submitted to the EMBL Data Library, November 1995
A;Reference number: Z1975
A;Reference number: Z1975
A;Reference number: Z1975
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 SVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 EVLVAPAVPSCEVPSSALSGTVVELRCQDXEGNPAPEYTWPKDGIRLLENPRLGSQSTNS 166
                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1328 <M12>
A;Cross-references: EMBL:Z68006; PIDN:CAA91999.1; GSPDB:GN00028; CESP:K09C8.5
A;Experimental source: clone K09C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRL---LENPRLGSQSTNSSYTM 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 NTKTGTLQFNTVSKLDTGEYSCEARNSVGYR------RCPGKRMQVDDLNISGIIA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U80022; PIDN:AAC25886.1; GSPDB:GN00023; CESP:F12F3.2 A;Experimental source: strain Bristol N2; clone F12F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: T34416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 155.5; DB 2; Leus.
Pred. No. 0.0003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.0%; Score 155.5; DB 2; Best Local Similarity 30.4%; Pred. No. 0.00072; Matches 58; Conservative 15; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F12F3.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 SYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Statu8: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%;
27.5%;
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Matches 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-2783 <FUL>
                                                                                                                                                                                                                                                                                                                                                                                                       C, Genetics:
A, Gene: CESP: K09C8.5
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Cidate: 25-Nov-1997 #sequence revision 25-Nov-1997 #text_change 08-Sep-2002
Cidate: 25-Nov-1997 #sequence revision 25-Nov-1997 #text_change 08-Sep-2002
Cidate: 25-Nov-1997 #sequence revision 25-Nov-1997
Ridigashiyama, 5: #fortkawa, m.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag
J. Biochem. 122, 675-680, 1997
A;Title: A novel brain-derived member of the epidermal growth factor family that interact A;Accession: JC5701
A;Accession: JC5701
A;Molecule type: mRNA
A;Residues: 12868 + HIG-
A;Accession: PC4411
A;Accession: PC4411
A;Accession: PC4411
A;Accession: PC4412
Cioamental source: PC-12 cell
C;Comment: This protein is a member of the epidermal growth factor family. It is functic ating the differentiation of MDA-MB-453 cells.
C;Superfamily: human BrbB kinase activator alpha, brain and thymus; EGF homology; immuno F;361-397/Domain: EGF homology eEGF>
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                                                                                                                              LERNORYIFFLEPTEQPLVFKTAFAPVDPN--GKNI-KKEVGKILCTDCATRPKLKKMKS 260
                                                                                      44 LGRSVSFVYYQQTLQGD--FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEE 101
                                                                                                                                                                                       DIVILEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWPKDGIRLLENPRLGS 161
                                                                                                                                                                                                                                                                                           162 OSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNI----S 216
                                                                                                                                                                                                                                                                                                                         261 QTGEV-----SGEKOSLKCEAAAGNPQPSYRWFKDGKELNR----S 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 LGRSVSFVYYQQTLQGD--FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 DTVTLEVLVAPPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNI----S 216
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hypothetical protein K09C0.5 - Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
Cibacession: T23007, T23543

Rikershaw, J.
Submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ErbB kinase activator alphal, brain and thymus - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Nov_1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
                                                                                                                                                                                                                        Gaps
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                                     36;
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11.1%; Score 157; DB 2; Length 868;
Best Local Similarity 27.7%; Pred. No. 0.00014;
Matches 56; Conservative 24; Mismatches 86; Indels
                                     86; Indels
        Pred. No. 0.00014;
27.7%; Pred. .v..
                                                                                                                                                                                                                                                                                                                                                                                            217 GIIAAVVVVALVISVCGLGVCY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                356 GHARKCNETAKSYCVNG-GVCY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIIAAVVVVALVISVCGLGVCY 238
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                                   Conservative
             Best Local Similarity
                                                                                                                                                                                                                                           261 QTGEV----
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A;Reference number: 865939; MUID:95354678; PMID:7628460
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A)Experimental source: strain BALB/c
A)Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A)Note: only a part of the coding sequence is given
C;Comment: This protein is expressed at the cell surface and plays a determinant role
                                                                                                                                            44 LGRSVSFVYYQQTLQGD--FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEE 101
                                                                                                                                                                                                                                                                                                                                 245 QTGQV-----GEKQSLKCEAAAGNPQPSYRWFKDGKELNR----S 280
                                                                                                                                                                                                                                                                                                                                                                                                                             QSTNSSYTMINTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNI----S 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 LEEDTVTLEVLVAPAVPSCEVPSSAL--SGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---DPFSLNIIYGPDTPIIS-PSDIYLHPGSNLNLSCH-AASNPPAQYFWL----INEK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFN--IRIKNVTRSDAGKYRCEVSAPSEQGQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: JC1508
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-521 cMCC>
A;Cross-references: EMBL:X67279; NID:g50170; PIDN:CAA47696.1; PID:g50171
A;Experimental source: strain CD1; tissue colon
R;Modellec, P.; Turbide, C.; Beauchemin, N.
Eur. J. Blochem. 231, 104-114, 1995
A;Title: Characterization and transcriptional activity of the mouse bilis
                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 119;
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Length 850;
                                                                      86; Indels
10.9%; Score 155; DB 2; 27.7%; Pred. No. 0.00019; tive 24; Mismatches 86,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 GHARKCNETAKSYCVNG-GVCY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIIAAVVVVALVISVCGLGVCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-21 <NED>
                                    Similarity 27.79
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 70; Conserv
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A;Gene: BgpD; bgp1
                                                                      26;
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                                                                                                                                                                                                                                                                                 102
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Query Match
Best Local 8
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C; Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
C; Accession: JG5700
R; Higashiyama, S; Horikawa, M; Yamada, K; Ichino, N; Nakano, N; Nakagawa, T; Miyag
J; Blochem. 122, 675-680, 1997
A; Title: A novel brain-derived member of the epidermal growth factor family that interact
A; Reference number: JG5700; MUID: 98006324; PMID: 9348101
A; Reference number: JG5700
A; Residues: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-850 A: HIG.
A; Molecule type: mRNA
A; Residues: 1-850 A: HIG.
A; Comment: This protein is a member of the epidermal growth factor family. It is functic
C; Superfamily: human BrbB kinase activator alpha, brain and thymus; EGF homology; immunc
C; Reywords: glycoprotein
F; 258-311/Domain: Ig-like #status predicted A: B; 346-381/Domain: EGF homology A: B; 346-381/Domain: EGF homology A: B; 346-381/Domain: EGF homology A: B; 147,278,451/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 147,278,451/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                               Cider: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
Cider: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
Cidecession: J0100
Cidecession: J0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIRMSALTLKDIQYTDAGEYFCVASNPI----GVDMQAMYFEVQYAPKIRG-PVVVYTW 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | | : | : | : | : | : | : | EGNPUNITC-DVLAHPSAAVSWFRDG-QILPS----SNFSNIKIYNGPTFSSLEVNPDSE 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 FSAPKDQQV---VTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFKNR 64
                                                                                                                                                                                                                                                                                                                                        Species: Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ErbB kinase activator alpha, brain and thymus - human
C;Species: Homo sapiens (man)
C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.9%; Score 155; DB 2; Length 725; Best Local Similarity 26.6%; Pred. No. 0.00016; Matches 55; Conservative 37; Mismatches 99; Indels
                                                                                                                                                                                                                                                                  eural cell adhesion molecule 2 - African clawed frog Alternate names: N-CAM 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | : | | | | : | : | NDFGNYNCSAVNSIGHESSEFILLVQAD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 LDTGEYSCEARNSVGYRRCPGKRMQVD 211
                                                                      || |:||:
2768 FSVVHVLLISI 2778
                                 231
                             AVVVVALVISV
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Search completed: December 9, 2003, 17:13:42 Job time : 14.9443 secs

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December 9, 2003, 17:08:11 ; Search time 9.13589 Seconds (without alignments) 1420.702 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                     OM protein - protein search, using sw model
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US-09-852-797-76_COPY_23_298 1418 1 YHKAYGFSAPKDQQVVTAVX.......SSKATTMSENDFKHTKSFII 276 Title: Perfect score: Sequence:

127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SITMMARTES

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO SECONDARY LYMPHOID ORGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 YHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                            SUBCELLULAR LOCATION: Type I membrane protein (Potential). TISSUB SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS. LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
                                                                                                      SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
DATABASE: NAME-EROW; NOTE-PROW 2:1-3(2001);
WWW-nttp://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [mmunoglobulin domain; Glycoprotein; Transmembrane; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JUNCTIONAL ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          MIM; 606870; -. Cintegral to plasma membrane; NAS. GO; 0005887; C:integral to plasma membrane; NAS. GO; GO:0016337; P:cell-cell adhesion; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig_C2. InterPro; IPR033006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
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Pred. No. 3.8e-113;
0; Mismatches 2;
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IG-LIKE C2-TYPE.
POTENTIAL.
POTENTIAL.
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EMBL; AY016009; AAG49022.1; -.
EMBL; BC017779; AAH17779.1; -.
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SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
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298 AA;
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MIM; 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wiemann S., Weil B., Weilenther R., Gassenhuber J., Glassl S., Wiemann S., Weil B., Weilenther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterehoeft A., Beyer A., Kochrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Mambutt R., Korn B., Klein M., Poustka A.;

"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";

"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";

"Towards a catalog of human genes and proteins sequencing and recruits PARD3. The association of the PARO6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing recruits PARD3. The association of the PARO6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing right junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.

-1- SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this interaction (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERPAMILY.

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          redistribution
                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion molecule 1) (PAM-1) (Platelet F11 receptor).
F11R OR JAM1 OR JCAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Naik U.P., Naik M.U., DeLeon P., Spychala J.;

"Cloning and characterization of PAM-1, a novel platelet adhesion molecule involved in platelet activation.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINES99313940; PubMed=10395639;
Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.
Iwamatsu A., Kita T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss
                                                                                                                                                                                                                                                                                                                                                                                                  "Combined treatment of TNF-alpha and IFN-gamma causes redistrible junctional adhesion molecule in human endothelial cells.", J. Immunol. 163:553-557(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel Ig superfamily member from human platelets.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and sequencing of the cDNA of
  299 AA.
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  STANDARD;
                                                                                                                                                                                        Homo sapiens (Human)
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JAM1 HUMAN
Q9Y624;
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DISULPID
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MEDLINE=99323940; PubMed=10395639;
Ozaki H., Ishli K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
Ishli K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
"Combined treatment of TNF-alpha and IFN-gamma causes redistribution
of junctional adhesion molecule in human endothelial cells.";
                                                                                Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
D95DE2FEA23D2851 CRC64;
                                                                                                                                                                                                                                                                                              40,
                                                                                                                                                                                                                                                                        ; DB 1; Length 299; 4.7e-29;
                                                                                                                                                             JUNCTIONAL ADHESION MOLECULE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                           99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 RKGYFSKETSFOKSNSSSKA----TTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEGHFORT --- KKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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IG-LIKE V-TYPE 2.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Junctional adhesion molecule 1 precursor (JAM)
                                                          GO: GO:0006954; P:inflammatory response; TAS
                                                                                                                                                                                                                                                                                 35.6%; Pred. No. 4.7e
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EMBL; AF207907; AAF22829.1; -. EMBL; AF172398; AAD48877.1; -. EMBL; AL136649; CAB66584.1; -.
                                                                                                                                                                                                                                                     32583 MW;
                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
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Matches 100; Conservative
                              PIR; A59406; S56749.
Genew; HGNC:14685; F11R.
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299 AA;
                                                 MIM; 605721; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR0071051 g-like.
InterPro; IPR007100598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfan; PPR0047; ig_. 2.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane; SIGNAL 1.
SIGNAL 1.
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CYTOPLASMIC (POTENTIAL).
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IG-LIKE V-TYPE 2.
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163:553-557 (1999).
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2398 JU
237 EX
258 PC
298 CY
224 IG
227 IG
227 IG
211 PP
32456 MW,
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RESULT 4 JAMI_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P., Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T., Winkler F.K., Hennig M.;

Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T., Winkler F.K., Hennig M.;

"X-ray structure of junctional adhesion molecule structural basis for homophilic adhesion via a novel dimerization motif.";

EMBO J. 20:4391-4398 (2001).

-1- FUNCTION: Seems to plays a role in epithelial tight junction recruites PARD: The association of the PARDs and recruites PARD: The association of the PARDs and the PARDs complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly. Plays a role in regulating monocyte transmignation involved in integrity of epithelial barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simmons D., Dejana E.; "Junctional adhesion molecule, a novel member of the immunoglobulin superfamily that distributes at intercellular junctions and modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Marcin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano
Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interaction.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
Localized at tight junctions of both epithelial and endothelial
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Involved in platelet activation.
SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ebnet K., Suzuki A., Horikoshi Y., Hirose T., Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.; "The cell polarity protein ASIP/PAR-3 directly associates with junctional adhesion molecule (JAM)."; EMBO J. 20:3738-3748(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: Localized at tight junctions of both epithelial and endothelial cells.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238
                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
FIR OR JAM1 OR JCAM1 OR JCAM.
300 AA
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monocyte transmigration.";
J. Cell Biol. 142:117-127(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 1F97; 22-AUG-01.
MGD; MGI:1231398; F11r.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
PFam; PPR0047; Ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U89915; AAC32982.1; -
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH PARD3.
                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11447115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11500366;
JAM1 MOUSE
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185 LDTGEYSCEARNSVG-YRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 EMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGONLEEDTVTLEVLVAPAVPSCEVPSSALS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 GTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQS-TNSSYTWNTKTGTLQFNTVSK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                           7 FSAPKDOQVVTAVXYQEAILACKTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRA 65
                                                                                                                                                                                                                                                                                                                                                                         12; Gaps
Tight junction, Immunoglobulin domain, Glycoprotein, Transmembrane, Repeat; Signal, 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The human A33 antigen is a transmembrane glycoprotein and a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Colon carcinoma;
MEDLINE=97165045; PubMed=9012807;
MEDLINE=97165045; PubMed=9012807;
Meath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
Burgess A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of posttranslational modifications of human A33 antigen, a novel palmitoylated surface glycoprotein of human gastrointestinal epithelium.";
                                                                                                                                                                                                                    212 POTENTIAL.
42 N-LINKED (GLCNAC. . .) (POTENTIAL)
8185 N-LINKED (GLCNAC. . .) (POTENTIAL)
32368 MW, 391F3E48FF3B97EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POST-TRANSLATIONAL MODIFICATIONS.
MEDLINE=97396159; PubMed=9245713;
Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
                                                             JUNCTIONAL ADHESION MOLECULE 1.

BYERACELULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE V-TYPE 2.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                              DB 1; Length 300;
                                                                                                                                                                                                                                                                                                                            28.9%; Score 410; DB 1; Length 300; 35.9%; Pred. No. 1.1e-27; Live 49; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cell surface A33 antigen precursor (Glycoprotein A33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 YF---SKETSFOKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFETTKKGTAPGKKVIYSQPSTRSEGEFKQTSSFLV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nember of the immunoglobulin superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                 Local Similarity 35.9% tes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                   300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpson R.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GD-FKNR-----AEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDT----VTLEV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKNISTDT------SGYYICTSSNEEGTQFCNITVAVRSPSMAVALYVGIAVGVVA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 TMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCP-GKRMQVDDLNIS------GIIA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPKDQQVVTAVXYQEAILACKTPKKTVXSR---LEWKKL-----GRSVSFVYYQQT-LQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chem. Biophys. Res. Commun. 236:682-686(1997).
FUNCTION: MAY PLAY A ROLE IN CELL-CELL RECOGNITION AND SIGNALING.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN NORMAL GASTROINTESTINAL
EPITHELIUM AND IN 95% OF COLON CANCERS.
PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                              OCO, GO: 0005889; C:proteoglycan integral to plasma membrane; TAS. GO; GO: 0004872; F:receptor activity; TAS. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_W. PF00047; Ig; 2. SMART; SM00406; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
N-LINKED (GLCNAC. ..) (POTENTIAL)
...TNKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                              PTM: PALMITOYLATED.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; ĬĠv; 1.
PROSTER; PSS0815; IG LIKE; 2.
Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
Transmembrane; Signal; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 2e-12;
41; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKED (GLCNAC. . .) (PC 9BFC7AAF45C2408E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SURFACE A33 ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
POLY-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.3%; Score 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35632 MW;
                                                                                                                                                                                                                                                                     EMBL; U79725; AAC50957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.6%;
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nes 72; Conservative
                                                                                                                                                                                                                                                                                    Genew; HGNC:4445; GPA33.
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319 AA;
                                                                                   CARBOHYDRATE.
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236
257
257
257
258
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TRANSMEM
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DOMAIN
DOMAIN
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A REDLINE-2238257; PubMed=12477932;

RX MEDLINE-2238257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altaner R.D. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Waxs I.T., Wang J., Halte F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunarane P.H.,

R Richards S.S., Morley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Sthards S., Worley M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RY "Generation and initial analysis of more than 15,000 full-length

RY Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomko R.P., Xu R., Philipson L.;
"HCAR and MCAR: the human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses.";
Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M., Sollerbrant K., Sonnhammer E., Philipson L.; "Putative regulatory domains in the human and mouse CAR genes."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                     R.W.
                                                                                                                   ä
                                                                                                                                                                                               Dokaro saprota; Michara; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                   (Coxsackievirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic organization and chromosomal localization of the human Coxsackievirus B-adenovirus receptor gene.";
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILTRE=91990109; PubMed=9036860;
MEDILTRE=9190109; PubMed=9036860;
MEDILTRE=9190109; M.A., Cunningham J.A., Droquett G., Kurt-Jones E.,
Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg
"Isolation of a common receptor for Coxsackie B viruses and
adenoviruses 2 and S.";
Science 275:1320-1323(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.; "Sequence and expression of CXADR, the human gene for the coxsackievirus and adenovirus receptor."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20008750; PubMed=10543405;
Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
Bowles N.E.;
CXAR HUMAN STANDARD; PRT; 365 AA.
P78310; 000694;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
cosackievirus and adenovirus receptor precursor (Cocackievirus receptor) (hCAR) (CVB3 binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97250541; PubMed=9096397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genet. 105:354-359(1999)
                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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RESULT 7
FAS2_DROME
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 QQTLQGDF-----KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 KIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLOYEWQK-----LSDSQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIA-A 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
EXTRACELULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AYGFSAPKDQQVVTAVXYQEAILACK---TPKKTVXSRLEW------KKLGRSVSFVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Mismatches 117; Indels 39; Gaps
-!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%; Score 190.5; DB 1; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.4e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                              AF200465, AAF24344.1; -.
AF242865, AAG01088.1; -.
AF242864; AAG01088.1; JOINED.
AF242864; AAG01088.1; JOINED.
                                                                                                                                                                                                                                                                                    BC003684; AAH03684.1; -.
BC010536; AAH10536.1; -.
EAJ; 13-JUL-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40029 MW;
                                                                                                                                           EMBL; Y07593; CAA68868.1; -. EMBL; U90716; AAC51234.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.5%;
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MIM; 602621; -.
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237
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PDB; 1F5W; 08-NOV-00.
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201
365 AA;
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les 64; Conserv
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DD 183 NOFFSKIALANGENISTERSTORTSCHANKUGSDOCLARIANVEPSKKAGIAGA 242

222 VVVALVISVCGLOVCHAGRACHFSKETSCR 233

DA 222 VVVALVISVCGLOVCHAGRACHFSKETSCR 233

DA 223 PROBER STANDAD:

PRESIDENT TO THE STANDAD:

PRESIDENT
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CHAIN
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LECALMS

LECLALMS

LECLALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Neuronal recognition molecule for the MP1 axon pathway, pathway recognition for axons during the development of nerve
               REVISIONS, AND ALTERNATIVE SPLICING.
STRAIN-Berkeley;
MEDLINE=22426069; PubMed=12537572;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Barman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Staplecon M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                           MEDLINE-Z019601-R;
MEDLINE-Z0196011; PubMed=10731137;
MEDLINE-Z0196011; PubMed=10731137;
Bernos P. V., Gatt M. K., Ashburner M., Murphy L., Harris D., Bernos P. V., Catt M. K., Ashburner M., Brun C., Demailles J., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D., Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Campbell L.A., Darlamitsou A., Henderson N.S., Momilian P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=1;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "From sequence to chromosome: the tip of the X chromosome of D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLUIAR LOCATION: Type I membrane protein (isoform 1); attached to the membrane by a GPI-anchor (isoform 2). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                  Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; ALO33125; CAA21825.1; -.
EMBL; AE003430; AAF45925.2; -.
EMBL; AE003430; AAF45925.2; -.
EMBL; AE003430; AAR09119.1; -.
EMBL; AL033125; CAA21826.1; -.
EMBL; AL033125; CAA21826.1; -.
EMBL; AL03125; CAA21826.1; -.
FlyBase; FBgn0000635; Fas2.
GO; GO:000156; P:homophilic cell adhesion; IDA.
GO; GO:0007611; P:learning and/or memory; IMP.
GO; GO:0016319; P:learning and/or memory; IMP.
GO; GO:0016319; P:neushroom body development; IMP.
GO; GO:001838; P:neuronal cell recognition; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M77165; AAA28527.1; -.
EMBL; M77166; AAA28528.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster.";
Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 22-873 FROM N.A.
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62 KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGONLEEDTVTLEVLVAPAVPSCEVPS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 SALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 VSKLDTGEYSCEARNSVGYRRCPGK-----RMQVDDL-NISGIIAAVVVVALVISVCGLG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Çi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITTATTIITLATTISITLLSVLASMLA (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDVIQVAERQVESSAAIVGIAIGGVLLLLFVVDLLCCITVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||::|
142 NAPENQYPTLG---QDYVVMCEVKADPNPTI----DWLRNGDPIRTTNDKYVVQT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 SAPKDOOVVTAVXYQEAILACKT---PKKTVXSRLEWKKLG---RSVSFVYYQQTLQGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 -----NGLLIRNVQESDEGIYTCR-AAVIETGELLER-TIRVEVFIQPEIISLPTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIDVIQVAERQVFSSAAIVGIAIGGVLLLLFVVDLLC
DNPHPSTSGAAPLAQLLVIFTALPTMLLILPPTTHTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        C. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 873;
          InterPro; IPR003861; FN III.
InterPro; IPR003861; FN III.
InterPro; IPR003066; Ig-1ike.
InterPro; IPR003006; Ig-Mc.
InterPro; IPR003006; Ig-Mc.
InterPro; IPR0041; ig. 2.
Pfam; PF00041; ig. 2.
SWART; SW00040; IGC2; 3.
SWART; SW00408; IGC2; 3.
PROSITE; PS50835; IG_LIKE; 5.
Cell adheaion; Glycoprotein; Repeat; Alternative splicing; Immunoglobulin domain; Transmembrane; GPI-anchor; Signal;
30; GO:0045473; P:response to ethanol (sensu Insecta); NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Missing (In isoform 2).
/FTId=VSP 002509.
S -> R (IN REF. 4; CAA21826).
E48F0484CCE62AC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Conservative 50; Mismatches 101; Indels
                                                                                                                                                                                               FASCICLIN II.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (in isoform 3).
                                                                                                                                                                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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4.5e-08;
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(GLCNAC.
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N-LINKED
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                                                                                                                                                                      Neurogenesis.
SIGNAL
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us-09-852-797-76_copy_23_298.rsp

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DISULFID
DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                    Tomko R.P., Xu R., Philipson L.;
"HCAR and MCAR: the human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses.";
Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 2. SMART; SM00408; IGc2; 1. PROSITE; PS50815; IG LIKE; 2. Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                             STRAIN=CS7BL/6J; TISSUE=Liver;

MEDLINE=97190109; PubMed=9036860;

Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,

Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;

"Isolation of a common receptor for Coxeackie B viruses and
schenoviruses 2 and 5.";

Science 275:1320-1322 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                 CXAR_MOUSE STANDARD, PRT; 365 AA.
P97792; 009052;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
COXBACKIEVIALS and adenovirus receptor homolog precursor (mCAR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMOLOG.
EXTRACELLULAR (POTENTIAL)
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
236 VCYAQRKGYFSKETSFQKSNSSSKATTMSEND 267
                342 TCRA--KGRPAPAITFRRWGTQEEYTNGQQDD 371
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MEDLINE=97250541; PubMed=9096397;
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EMBL; U90715; AAC53148.1; --
EMBL; Y11929; CAA72679.1; --
MGD; MGI:1201679; Cxadr.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Ig_C2.
InterPro; IPR033006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AAVVV---VALVISVCGLGVCYAQR-------KGYFSKETSFQKSNS 256
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
VAAPNISRAGAVPVMIPAQKEDGSIV -> FKYAYKTDGIT
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                                                                                                                                                                                                                                                                                              6 GFSAPKDQQVVTAVXYQEAILACK---TPKKTVXSRLEW-----KKLGRSVSFVY---
                                                                                                                                                                                                                                                                                                                                         19 GLSITTPEQRIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPSDNQIVDQVIILYSGDK
                                                                                                                                                                                                                                                                                                                                                                                            ----YQQTLQGDF---KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 SSYTMNT-----KTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGII
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Structural component of the muscle M-line. Myofilament
lattice assembly begins with positional cues laid down in the
basement membrane and muscle cell membrane. UNC-89 responds to
these signals, localizes, and then participates in assembling an
M-line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96180279; PubMed=8603916; Benian G.M., Tinley T.L., Tang X., Borodovsky M.; Tinley T.L., Tang X., Borodovsky M.; The Caenorhabditis elegans gene unc-89, required for muscle M-line assembly, encodes a giant modular protein composed of Ig and signal transduction domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UN89 CAEEL STANDARD; PRT; 6632 AA.
001761, 017362, 12.
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Muscle M.line assembly protein unc-89 (Uncoordinated protein 89)
UNC-89 OR COSDI.1.
                                                                                                                                                                                           12.7%; Score 180; DB 1; Length 365;
23.7%; Pred. No. 5e-08;
ive 44; Mismatches 130; Indels 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Bristol N2;
Du Z., Le T.T., Wilson R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                       VV (IN REF. 2 AND 3).
5445B4B52A34B2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell Biol. 132:835-848(1996).
                                                                                                                                                365 AA; 39947 MW;
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3813 GRGAPEFVELLRSCTVTEKQQAILKCKV-KGEPRPKIKWTKEGKEVEM-----SAR
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       | IG-LIKE C2-TYPE 22. |
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| IG-LIKE C2-TYPE 24. |
| IG-LIKE C2-TYPE 24. |
| IG-LIKE C2-TYPE 25. |
| IG-LIKE C2-TYPE 26. |
| IG-LIKE C2-TYPE 29. |
| IG-LIKE C2-TYPE 29. |
| IG-LIKE C2-TYPE 31. |
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| IG-LIKE C2-TYPE 31. |
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| IG-LIKE C2-TYPE 34. |
| IG-LIKE C2-TYPE 36. |
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| IG-LIKE C2-TYPE 37. |
| IG-LIKE C2-TYPE 40. |
| IG-LIKE C2-TYPE 41. |
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                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE SPECIFICITY: Localizes to the middle of A-bands.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 fibronectin type III domain.
SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 5 RCSD domains.
SIMILARITY: Contains 1 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U33058; AABO0542.1;

R PDB; 1PHO; 20-DBC-00.

R Wormeep; CO9D1.1; CA34426.

R InterPro; IPR003961; FN III.

R InterPro; IPR003106; Ig_MAC.

R InterPro; IPR003066; Ig_MAC.

R InterPro; IPR001006; Ig_MAC.

R InterPro; IPR001006; Ig_MAC.

R InterPro; IPR001019; RhoGE.

R InterPro; IPR00141; fn3; 1.

R Pfam; PF00041; fn3; 1.

R Pfam; PF00047; ig; 47.

R Pfam; PF001018; SH3; 1.

R Pfam; PF001018; SH3; 1.

R Pfam; PF001018; SH3; 1.

R PARRT; SM00325; RhoGEF; 1.

R PROSITE; PS50010; DH 2: 1.

R PROSITE; PS50010; DH 2: 1.

R PROSITE; PS50010; DH 2: 1.

R PROSITE; PS50003; PH DOMAIN; 1.

R PROSITE; PS50010; DH 2: 1.

R DOMAIN 152 330 DH.

T DOMAIN 342 498 PH.

T DOMAIN 342 498 PH.

T DOMAIN 648 338 IG-LIKE C2-TYPE 3.

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T DOMAIN 648 838 IG-LIKE C2-TYPE 3.

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C2-TYPE 8.
C2-TYPE 10.
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DH.

PH.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 6.

THR-RICH.

RCSD 1.

RCSD 2.

RCSD 3.

RCSD 3.

RCSD 5.
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PDFLQPVKPAVVTVGETAVLEGKI-----SGKPKPSVKWYKNGEELKPSDRVKIE-- 3969
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RX MEDLINE=22388257; PubMed=12477932;
RA Attauencr R.D., Collins F.S., Wagner L.H., Derge J.G., Schuler G.D., RA Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diachenko L., Marueina K., Farmer A.A., Rubin G.M., Hong L. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Stapleton M., Soares M.B., Bonaldo M.F., Carannor R.D., Mullah F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., ugdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., McKernan K.J., Malek J.A., Gunarane P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W., R. Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W., RA Wilting M., Madan A., Young A.C., Shevchenko Y., Butfard G.G., Sheny J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A. RA Blakesley R.W., Touchman J.W., Scheurz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., R. Willen and initial analysis of more than 15,000 full-length R. Proc. Natl. Acad. Sci. U.S.A., 99:16809-16903(2002).

C. -- SUBCELLULAR LOCATION. Attached to the membrane by a GPI-anchor. C. -- SIBERBAILY. EBALONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CEA
-----SSALSGTVVELRCQDKEGNPAPEYTWPKDGIRLLENPRLGSQST 164
                                                                                                                                                                                                                                              CEAG HUMAN STANDARD; F..., P40199; 014920; 014920; 0178E-1995 (Rel. 31, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 42, Last annotation update) 15-SEP-2003 (Rel. 42, Last annotation update) Carcinoembryonic antigen-related cell adhesion molecule 6 precursor carcinoembryonic antigen) (Nonspecific crossreacting antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=89122014; PubMed=3220478;
MEDLINE=89122014; PubMed=3220478;
Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
"Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and CEA and suggestion of nonrandom sequence variation in their conserved loop-domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Lung carcinoma, MEDLINE=88106638; PubMed=3337731; MEDLINE=88106638; PubMed=3337731; MEDLINE=88106638; PubMed=3337731; MEDLINE=88106638; MATSUORA Y., KOSBKI G., NAKAZATO H.; MPTIMARY STRUCTURE OF IONSPECIALIC CROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                           3970 -----NLDDGTQRLTVTNAKLDDMDEYRCEASNEFG 4000
                                                                                            165 NSSYTMUTKTGTLQFN-TVSKL-DTGEYSCEARNSVG
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 DFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSA--LSG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 TVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                              CARCINOEMBRYONIC ANTIGEN-RELATED CELL ADHESION MOLECULE 6. REMOVED IN MATURE FORM (BY SIMILARITY). GPI-ANCHOR (BY SIMILARITY).
                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 2.
Immunoglobulin domain; Antigen; Signal; Glycoprotein; GPI-anchor;
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EMBL; M18729; AAA59907.1; -...
EMBL; BC005008; AAH05008.1; -...
GPBL; BC005008; AAH05008.1; -...
GP; GO:0005890; -...
GO; GO:0005897; C:integral to plasma membrane; TAS.
GO; GO:0007167; P:cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
INTERPRO; IPR00110; Ig-like.
InterPro; IPR003106; Ig-MHC.
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V -> G (IN REF. 1).
4322C5D6E25849F5 CRC64;
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
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(Rel. 29, Last sequence update)
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29.0%; Pred. No. 1
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SMART; SM00408; IGc2; 1.
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EMBL; X70842; CAA50192.1;

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15-SEP-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor receptor 2 precursor (BC 2.7.1.112)
(VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93141255; PubMed=8423988; Octivible R., Wilks A.F.; Octivible R.B., Reid H.H., Bernard O., Ziemiecki A., Wilks A.F.; NYK/FLK-1: a putetive receptor protein tyrosine kinase isolated from ElO embryonic neuroepithelium is expressed in endothelial cells of
                                                                                                                                                                                                                                                                                                                                                          "A receptor tyrosine kinase cDNA isolated from a population of entriched primitive hematopoietic cells and exhibiting close genetic linkage to c-kit:";
Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-15 FROM N.A.
MEDLINE=96032749; PubMed=7559454;
Patterson C., Perrella M.A., Høieh C.-M., Yoshizumi M., Lee M.-E.,
                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and functional analysis of the promoter for KDR/flk-1, a receptor for vascular endothelial growth factor."; J. Biol. Chem. 270:23111-23118(1995).
                                                                                                                                                              STRAIN=BALB/c; TISSUE=Embryo;

MEDLINE=29208880; PubMed=7681362;

Millauer B., Wizigmann-Voos S., Schnurch H., Martinez R.,

Mueller N.P.H., Risau W., Ullrich A.;

Mueller N.P.H., Risau W., Ullrich A.;

Migh affinity VEGF binding and developmental expression suggest

Flk-1 as a major regulator of vasculogenesis and angiogenesis.";
                                                                                                                                                                                                                                                                                             STRAIN=C3H/He; TISSUE=Fetal liver;
MEDLINE=92020984; PubMed=1717995;
Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.
Lemishcka I.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93361481; PubMed=8356051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the developing embryo.";
Oncogene 8:11-18(1993).
                                                            FLK-1
                                                                          musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Quinn T.P., Peters K.G., de Vies C., Ferrara N., Williams L.T.,
"Fetal liver kinase 1 is a receptor for vascular endothelial growth
factor and is selectively expressed in vascular endothelium.";
Proc. Natl. Acad. Sci. U.S.A. 90:7533-7537(1993).
-!- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN
KINASE ACTIVITY. THE VEGF-KINASE LIGNAD/RECEPTOR SIGNALING SYSTEM
PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
VASCULAR PERMEABILLITY.

CATALITIC ACTIVITY: APP + a protein tyrosine = ADP + protein tyrosine phosphate.

tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT HEART, LUNG, KIDNEY, BRAIN AND SKELETAL MUSCLE, BUT IS ALSO EXPRESSED AT LOWER SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.

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PROSITE; PS00240; RECEPTOR TYR KINII; 1. Angiogenesis; Signal; Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; Phosphorylation; ATP-binding;
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N-LINKED (GLCNAC. .) (
PHOSPHORYLATION (AUTO-)
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
IG-LIKE C3-TYPE 7.
IG-LIKE C3-TY
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S -> C (IN REF. 1).
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G -> D (IN REF. 3)
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(GLCNAC.
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Pred. No. 1.1e-
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSSOB35; IG LIKE; 5.
PROSITE; PSOO107; PROTEIN KINASE ATP; 1.
PROSITE; PSOO119; PROTEIN KINASE DOM; 1.
PROSITE; PSOO109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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N-L
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                                                                                                                                                                                                      InterPro, IPR003598; Ig_c2.
InterPro, IPR003006; Ig_MHC.
InterPro; IPR000719; Prot kinase.
InterPro; IPR00184; RTKinase.
                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; 1g; 6.
Pfam; PF00069; pkinase; 1.
Pfam; PF000089; pkinase; 2.
SMART; SM00408; IGC2; 1.
SMART; SM00219; Tyrkc; 1.
                                                                                                                                                                                                                                                                                                         InterPro; IPR001245; Tyr_pkinase.
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24.8%;
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                  EMBL; X59397; CAA42040.1;
EMBL; S53103; AAB25043.1;
EMBL; X89777; CAA61917.1;
PIR; A41228; A41228.
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719
1057
25
679
784
917
                                                                                                                                                                           InterPro, IPR007110;
                                                                                                                                                                                                   InterPro; IPR003598;
InterPro; IPR003006;
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Best Local Similarity
Matches 53; Conservat
                                                                                                                        HSSP; P11362; 1FGK.
MGD; MGI:96683; Kdr
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SIGNAL
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TRANSMEM
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CARBOHYD
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AAB69125.1;

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EMBL; AF001287;
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                                                                                                                                    QEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFN------
                                                         EVSAPSEQGONLEEDTVTLEV
                                                                                    622 ILIVAFQNASLQDQGDYVCSAQDKKTKKRHCLVKQLIILERMAPMITG-NLENQTTTI--
                                                                                                                109 LVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSY
                                                                                                                                                                                                                                                                                       035136; 035962; Created)
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 36, Last annotation update)
Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell adhesion molecule) (R4912).
NCAM OR OR NCAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a novel neural cell adhesion molecule-related gene with a potential role in selective axonal projection.";
J. Biol. Chem. 272:26883-26086(1997).
-! FUNCTION: May play important roles in selective fasciculation and zone-to-zone projection of the primary olfactory axons.
-!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and attached to the membrane by a GPI-anchor (short isoform).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: EXPRESSED IN SUBSETS OF BOTH OLFACTORY AND TISSUE SPECIFICITY: EXPRESSED IN SUBSETS OF BOTH OLFACTORY AND VOMERONASAL NEURONS IN A ZONE-SPECIFIC MANNER. SIMILARITY: BELONGS TO THE INMUNOSLOBULIN SUPERFAMILY. SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
STRAINE-BALB/C, TISSUB-Olfactory neuroepithelium;
MEDLINE-973662; TISSUB-Olfactory neuroepithelium;
YOSHIHARA Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
Kagamiyama H., Mori K.;
"OCAM: A new member of the neural cell adhesion molecule family related to zone-to-zone projection of olfactory and vomeronasal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                         169 TMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRR 202
                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM SHORT).
STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
MEDLINE=97476194; PubMed=9334170;
Alenius.M., Bohm S.;
                                                                                                                                                                                                                                                                               837 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Long;
IsoId=035136-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurosci. 17:5830-5842(1997).
                                                         ---IRIKNVTRSDAGKYRC
                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                             NCM2 MOUSE
                                                                                                                                            619
                                                         72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              axons.";
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N-LINKED (GLCNAC...) (POTENTIAL).
T-LINKED (GLCNAC...) (POTENTIAL).
T-FNGLGLGALIGLOWALLLILVATDVSCFFIRQCGLLMC
ITRRMCGKKSGSSGKSKELEEGKAAYLKDGSKEPIVERRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 SVSFVYYQQTLQGDFKNR-AEMIDFNIRIKNVTRSDAGKYRCE--VSAPSEQGQNLEEDT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 VTLEVLVAPAV--PSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DERITNHEDGSPVNEPNETTPLTEPEKLPLKEENGKEVLNA
ETIEIKVSNDIIQSKEDDIKA -> NCCEANKGENGGQSWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRG2_RAT STANDARD; PRT; 868 AA.
035569; 035073; 035570; 035571;
15-DEC-1998 (Rel. 37, Created)
16-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2)
                               MGD; MGI:97282; Ncam...

A InterPro; IPR003961; FN III.

R InterPro; IPR003106; 1g_like.

R InterPro; IPR003106; 1g_MHC.

R InterPro; IPR003066; 1g_MHC.

R Ffam; PF00047; fig; 5.

R SMART; SM00060; FN3; 2.

R SMART; SM00408; 1G2.5

DR ROSITE; PS50835; 1G LIKE; 5.

DR PROSITE; PS60835; 1G LIKE; 5.

MR Cell adhesion; Transmembrane; Glycoprotein; Repeat;

KW Cell adhesion; Transmembrane; GPI-anchor; Alternative splicing.

KW Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNAVGFTFVITMSLSCLF (in isoform Short)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Indels
                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70473B053A2D65A5 CRC64;
                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 QSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 KGSNTELTVR-----NIINK-DGGSYVCKATNKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.2%; Score 159.5; DB 1
29.7%; Pred. No. 7.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROBABLE
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EMBL; AF001286; AAB69124.1;
EMBL; AF016619; AAC53375.1;
MGD; MGI:97282; Ncam2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 29.7% tes 47; Conservative
                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
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CARBOHYD
CARBOHYD
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DISULFID
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CARBOHYD
VARSPLIC
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NRG2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           844446
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PUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS, RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE ERBB RECEPTORS, MAY ALSO PROMITE THE HETERODIMERIZATION WITH THE EGF RECEPTOR. SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTECLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MYMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
           NRG2 OR NTAK.
Rattus norvegicus (Rat).
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                      novel brain-derived member of the epidermal growth factor family it interacts with ErbB3 and ErbB4."; Biochem. 122:675-680(1997).
                                                                                        SEQUENCE FROM N.A., SEQUENCE OF 128-162, AND ALTERNATIVE SPLICING, MEDLINE=98006324; PubMed=9348101; Higashiyama S., Horikawa M., Yamada K., Ichino N., Nakano N., Nakagawa T., Miyagawa J., Matsushita N., Nagatsu T., Taniguchi N., Ishiguro H.;
                                                                                                                                                                                                                                    MEDLINE=97311397; PubMed=9168114; Chang H., Riese D.J. II, Gilbert W., Stern D.F., McMahan U.J.; "Ligands for ErbB-family receptors encoded by a neuregulin-like gene."; Nature 387:509-512(1997).
 (Neural-and thymus-derived activator for ERBB kinases) (NTAK)].
                                                                                                                                                                                                             SEQUENCE OF 109-868 FROM N.A. (ISOFORMS 6 AND 7)
                                                                                                                                                                                                                         TISSUE=Cerebellum;
                                                                                                                                                                      that
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PYBRARATURE HOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

FYBRARATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=7;

Comment=Additional isoforms seem to exist. The alpha-type and beta-type differ in the EGF-LIKE domain;

Name=1; Synonyms=NTAK-alpha2A;

Isoid=035569-1; Sequence=bisplayed;

Name=2; Synonyms=NTAK-alpha2A;

Isoid=035569-2; Sequence=bisplayed;

Name=3; Synonyms=NTAK-beta;

Isoid=035569-2; Sequence=VSP_003471;

Name=4; Synonyms=NTAK-beta;

Isoid=035569-4; Sequence=VSP_003466, VSP_003471;

Name=5; Synonyms=NTAK-gamma;

Isoid=035569-5; Sequence=VSP_003467, VSP_003468;

Name=5; Synonyms=NTG2-alpha;

Isoid=035569-5; Sequence=VSP_003472, VSP_003468;

Name=5; Synonyms=NTG2-beta;

Isoid=035569-7; Sequence=VSP_003465, VSP_003473;

Name=7; Synonyms=NTG2-beta;

Isoid=035569-7; Sequence=VSP_003466, VSP_003473;

Name=7; Synonyms=NTG2-Peta;

Isoid=035569-7; Sequence=VSP_003466, VSP_003473;

Name=7; Synonyms-

DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTECLYTIC PROCESSING. REGULATION OF THE PROTECLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN +

DIMERIZATION (BY SIMILARITY).

DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).

PTM: PROTECLYIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR ÷

-

EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY) FORM (BY

SIMILARITY).
SIMILARITY: Contains 1 EGF-like domain. -

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                                                                                                                                                                                                                                                                                InterPro; IPR00510; EGF like.

InterPro; IPR00110; 1g-1ike.

DR InterPro; IPR00110; 1g-1ike.

DR InterPro; IPR00110; 1g-1ike.

DR InterPro; IPR001549; Neuregulin.

DR Fam; PF00008; EGF; 1.

DR Fam; PF00181; EGF; 1.

DR SWART; SM00181; EGF; 1.

DR SWART; SM00181; EGF; 1.

DR SWART; SM00181; EGF; 1.

DR ROSITE; PS00185; EGF 2; 1.

DR ROSITE; PS00185; IG 2: 1.

FT CHAIN 128 868 NEUREGUIN-2, MEMBRANE THAIN 128 868 NEUREGUIN-2.

FT CHAIN 128 429 EXTRACRITY.

FT TRANSMEM 430 450

FT DOMAIN 451 0.

THOMAIN 451 0.
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NGFFGQRCLEKLPLRLYMPDPKQ -> VGYTGDRCQQFAMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> VGYTG
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EXTRACELLULAR (POTENTIAL).
INTERNAL SIGNAL SEQUENCE (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (in isoform 2 and isoform 3).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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  -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGFFGQRCLEKLPLRLYMPDPKQKHLGFELKE
DRCQQFAMVNFSK (in isoform 4).
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PLV -> FFF (in isoform 3)
/FTId=VSP 003464
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/FTId=VSP 003467.
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/FTId=VSP_003469.
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Missing (in isofe
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POLY-PRO.
BY SIMILARITY.
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N-LINKED (GLCNI
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/FTId=VSP
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POLY-SER.
POLY-SER.
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                                                                                                                                                                                                                   EMBL; D89995; BAA23344.1; -. EMBL; D89996; BAA23345.1; -. EMBL; D89997; BAA23346.1; -. EMBL; D89998; BAA23347.1; -.
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WEDLINE=97342638; PubMed=9199335;

WEDLINE=97342638; PubMed=9199335;

WEDLINE=97342638; PubMed=9199335;

WARDIA S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J.,

Woolf E.A., Comrack C.A., Dussault B.J., Woolf J., Goodearl A.D.J.,

Gearing D.P.;

"Characterization of a neuregulin-related gene, Don-1, that is highly the expressed in restricted regions of the cerebellum and hippocampus.";

"Carresponderization of a neuregulin-related gene, Don-1, that is highly the cerebellum and hippocampus.";

"Carl. Biol. 17:4007-4014(1997).

"I expressed in restricted regions of the cerebellum and hippocampus.";

"I expressed in restricted regions of the cerebellum and hippocampus.";

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                             SVLWDTPGTGV
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                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Pro-neurequiin-2 precursor (Pro-NRG2) (Contains: Neuregulin-2 (NRG-2)
(Divergent of neuregulin 1) (DON-NJ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCB_TaxID=10090;
                                                                                                                                                                                                                                                                                        36;
                                            SSSQWSTSPSTLDIN (in isoform 6).
FYId=VSP 003472.
Missing (in isoform 6).
FYId=VSP 003473.
S -> F (IN REF. 2).
R -> H (IN REF. 2).
W; 3C7D4D94DBE64DE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A).
STRAIN-C5/BL/6; TISSUB-Brain;
MEDLINE=97311398; PubMed=9168115;
Carraway K.L. III, Weber J.L., Unger M.J., Ledesma J., Yu N.,
Gassmann M., Lai C.;
"Neuregulin-2, a new ligand of ErbB3/ErbB4-receptor tyrosine
                                                                                                                                                                                                                                         Length 868;
  /FTId=VSP_003471.
HLGFELKEAĒELYQKRVLTITGICVA ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S)
                                                                                                                                                                                                                                                                                      86; Indels
                                                                                                                                                                                                                                    11.1%; Score 157; DB 1;
llarity 27.7%; Pred. No. 1.3e-05;
Conservative 24; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        756 AA
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                                                                                                                                                                                       93776 MW;
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                                                                                                                                                                                       868 AA;
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Best Local Similarity
                        414
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NRG2 MOUSE
ID NRG2 MOUSE
AC P56974;
                                                                                                                                                                                                                                                                                 26;
                                                                                                                                      CONFLICT
CONFLICT
SEQUENCE
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                        VARSPLIC
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DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARITY).

DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                  FORM (BY SIMILARITY).
PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (In isoform NRG2-10).
/FTId=VSP 003461.
VGYTGDRCQOPAMVHPSKHLGFELKEAEELYQKRVLTITGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVALLVVG -- NGFFGGRCLEKLPLRLYMPDPKQSVLWDT
PGTGVSSSQWSTSPSTLDLN (in isoform DON-1S).
                                                                                                                                                                                 Isoid=P56974-4; Sequence=VSP_003460, VSP_003461;
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE BRAIN, WITH LOWER
LEVELS IN THE LUNG. IN THE CEREBELLUM, FOUND IN GRANULE AND
PURKINJE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                        -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI SIMILAKIII.
PRO-NENEGULIN-2, MEMBRANE-BOUND FORM.
NEUREGULIN-2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERNAL SIGNAL SEQUENCE (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE.
SER/THR-RICH.
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) (GLCNAC. . .) (POTENTIAL).
) (GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
--- SIMILARITY: Contains 1 EGF-like domain.
--- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
--- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
HSSP; Q12784; 1HRE.
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POLY-PRO.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTEN'

N-LINKED (GLCNAC. .) (PO
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                                                                                                    IsoId=P56974-2; Sequence=VSP_003464;
Name=DON-15; Synonyms=NRG2-5;
IsoId=P56974-3; Sequence=VSP_003462; VSP_003463;
Name=NRG2-10;
    Event=Alternative splicing; Named isoforms=4;
                         Comment=Additional isoforms seem to exist;
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                                                             Isold=P56974-1; Sequence=Displayed;
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InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
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FTId=VSP 003463.

ALTERNATIVE PRODUCTS

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                                                                                                                                                                                                                                  44 LGRSVSFVYYQQTLQGD--FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEE 101
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VGYTGDRCQOFAMVNFSKHLGFELKE -> NGFFGQRCLEK
LPLRLYMBDPKQK (in isoform DON-1M).
/FILd=VSP 003464.
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Genomics 43.43.51(1997).
-!- FUNCTION: MAY PLAY IMPORTANT ROLES IN SELECTIVE FASCICULATION AND
-!- FUNCTION: MAY PLAY IMPORTANT ROLES IN SELECTIVE FASCICULATION AND
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED MOST STRONGLY IN ADULT AND FETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paoloni-Giacobino A., Chen H., Antonarakis S.B., (Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                            86; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                         Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 2 precursor (N-CAM 2)
                                                                                                                              11.0%; Score 156; DB 1; 27.7%; Pred. No. 1.3e-05;
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GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0007158; P:neuronal cell adhesion; TAS.
InterPro; IPR003961; FN_III.
InterPro; IPR007110; Ig-like.
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MEDLINE=97369930; PubMed=9226371;
                                                                           82213 MW;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%; Score 155.5; DB 1; Length 837; 26.6%; Pred. No. 1.7e-05; ive 30; Mismatches 72; Indels 11;
                                                                                                                                     NEURAL CELL ADHESION MOLECULE 2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINKED (GLCNAC. . .) (PC C3D034106C5741C1 CRC64;
                                                                                                                                                                                         IG-LIKE C2-TYPE 1.
1G-LIKE C2-TYPE 2.
1G-LIKE C2-TYPE 3.
1G-LIKE C2-TYPE 4.
1G-LIKE C2-TYPE 5.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 1.
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(GLCNAC. . .)
(GLCNAC. . .)
InterPro; IPR003598; Ig_c2.
InterPro; IPR03006; Ig_MHC.
Pfam; PF00041; fi3, 2.
Pfam; PF00047; ig; 5.
SMART; SM00060; FN3; 2.
SMART; SM00408; IGC2; 5.
SMART; PS5085; IG_LIKE; 5.
Cell adhesion; Transmembrane; Glycoprotein; Repeat;
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(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q9YGH1 Q922D5 Q91665 Q91665 Q95120 Q95120 Q95120 Q95130 Q95130 Q91080	192109 19R067 ALIGNMENT	PRT;	Created) Last sequenc, Last annotat Can-associated protein) 2410030G21RIK ca; Craniata; (a; Sciurognati	521; g CC. -associ, r Is Lo s."; (2000).	, Du Pas an Emerg	, and Er 851; a K., Yo Y., Kor Kiyosav T., Bor
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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schridl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Fruruno M., Anon H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshaber B., K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM CONSORTIUM, Thus, The FANTOM CONSORTIUM, The RIKEN Genome Exploration Research Group Phase I & II Team; Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 YHKANGFSASKDHRQEVIVIEFQEAILACKIFKKITSSRLEWKKVGQGVSLVYYQQALQG
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YHKAYGFSAPKD-QQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                      Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                     298 AA; 33047 MW; 1124E0F07E6CF751 CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Junction cell adhesion molecule 2.
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STRAIN-C57BL/6J; TISSUE-SKin;
MEDLINE-22354683; PubMed=12466851;
                                                                                                                                                                                                         MACLE AF25531; AAF81224.;
EMBL; AA29757; CAC26699.1; -
EMBL; AK013914; BAB29053.1; -
EMBL; AK010616; BAB27064.1; -
MGD; MGI:1933820; JCam2.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 2. PROSITE; PS50835; IG_LIKE; 2.
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Matches 222; Conservative
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EMBL; AK078128; BAC37139.1; -. SEQUENCE 298 AA; 33182 MW; 1131F0BFD89CEB51 CRC64;
                                                                                                                                                                                                                        23 YHKANGPSASKDHRQEVTVIEFQEAILACKTPKKTTSSRLEWKKVGQGVSLVYYQQALQG
                                                                                                                                                                                            1 YHKAYGFSAPKD-QQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQG
                                                                                                                                                                                                                                                                                                       60 DFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                              Length 298;
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                                                                                                                                     Indels
EMBL; AK028757; BAC26102.1; -. SEQUENCE 298 AA; 33079 MW; CB8227EC13D349A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 ORKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
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                                                                           Query Match 81.5%; Score 1156; DB 11;
Best Local Similarity 79.8%; Pred. No. 1.2e-99;
Matches 221; Conservative 23; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Junction cell adhesion molecule 2.
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MEDLINE-STRENGE, TISSUE-Embryo;

MEDLINE-STRENGE, TISSUE-Embryo;

MEDLINE-STRENGE, Shihadea A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Mawai J., Shihadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Marawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Machi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Nachi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaert P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sabaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F,

Nyashiyaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanashiyaki V.
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STRAIN=CS7BL/6J; TISSUE=Mesonephros;
STRAIN=C354683; PubMed=12466851;
MEDLINE=2354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of Nature 420:563-573(2002).
EMBL; AJ300304; CAC20704.1; ---
EMBL; AX013156; BAB28683.1; ---
EMBL; AX013156; BAB28683.1; ---
EMBL; AX012156; BAB28699.1; ---
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                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-Mar-2003 (TrEMBLrel. 2, JAM-2 (1110002N23Rik protein)
(Junction cell adhesion molecule-2, JAM-2 (1110002N23Rik protein)
JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
262 QRKGYFSKETSFQKGSPASKVTTMSENDFKHTKSFII 298
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                                                                                                                                  310 AA
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MGD; MGI:1933825; JCam3.
InterPro; IPR007110; I9-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR03598; Ig_mHC.
                                                                                                                               PRELIMINARY;
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MEMBLINE-ZIUBS-660, PubMed=11217851,
A MEMBLINE-ZIUBS-660, PubMed=11217851,
A Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Azawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Askai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Maniya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whishaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Havashizaki V.
                                                                                                                                                                                                     TRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKE 137
                                                                                                                                                                                                                                                                                    138 GNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNS 197
                                                                                                                                                                                                                                                                                                                                                                 225 AGAARCEGQDMEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKS 284
                                                                                                                                                                                21 YOEAILAC-KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
NCBI_TaxID=10090;
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                                                                                                   Query Match
34.4%; Score 487.5; DB 11; Length 310;
Best Local Similarity 39.1%; Pred. No. 3.3e-37;
Matches 104; Conservative 55; Mismatches 96; Indels 11;
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain.
SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;
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STRAIN=C57BL/6J; TISSUE=Small intestine;
MEDLINE=21085660; PubMed=11217851;
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JCAM3 OR JCAM2 OR 1110002N23RIK.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK008187; BAB25519.1; -
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MGD; MGI:1933825; Jcam3.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig_c2.
InterPro; IPR003006; Ig_MHC.
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01-JUN-2001
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InterPro; IPR003006; Ig_MHC.
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Best Local Similarity
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01-DEC-2001
01-DEC-2001
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SEQUENCE
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Q96FL1
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                                                                                                                                                                                                                                                                                   78 TRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKE 137
                                                                                                                                                                                                                                                                                                                                                                                    138 GNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNS 197
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                                                                                                                                                                                                                                                      21 YQEAILAC-KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNV 77
                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                          11;
                                                                                                                                                34.3%; Score 486.5; DB 11; Length 310; 39.1%; Pred. No. 4.1e-37; Indels 11; Length 310; ive 54; Mismatches 97; Indels 11;
Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PSS0083; IG_LIKE; 2.
Immunoglobulin domain.
SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1110002N23Rik protein.
JCAM3 OR JCAM2 OR 1110002N23RIK.
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EMBL; AK003326; BAB22715.1; -
MGD; MGI:1933820; JCam2.
MGD; MGI:1933825; JCam3.
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InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                    Matches 104; Conservative
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                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 AGAARCEGQDMEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKS 284
                                                                                                                                                                                                                                                                                                                                                                    78 TRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKE 137
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                                                                                                                                                                                                               Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                               11;
                                                                                                                                                           DB 11; Length 310;
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                                                                                                                                                                                                            96; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Straubberg R.;
Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010690; AMH10690.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MC.
Pfam; PP00447; ig; 2.
SWART; SM0448; IGc2; 1.
Hypothetical protein; Immunoglobulin domain.
                                                                                                          6692BCAD68EA4B1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;
                                                                                                                                                        Query Match
34.2%; Score 484.5; DB 1:
Best Local Similarity 39.1%; Pred. No. 6.2e-37;
Matches 104; Conservative 55; Mismatches 96,
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Pfam; PF00047; ig; 2. —
SWART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Immuncglobulin domain.
SEQUENCE 310 AA; 34819 MW;
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198 VGYRRCPGKRMQVDDLAISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE--TSFQ- 252
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Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;

"Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Τ.;
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EMBL, AP356518; AAK27221.1; -..

EMBL, AJ34431; CAC69945.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Junctional adhesion molecule 3 precursor (Junctional adhesion molecule-2) (Junctional adhesional molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein FLJ90828).
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"Junctional adhesion molecules (JAMs) and interendothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cunningham S.A., Arrate M.P., Tran T.M.; "Cloning of Human Junctional Adhesion Molecule 3."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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Sache U.J.H., Eva O., Berghoefer H., Santoso S.;
"Characterization of Junctional Adhesional Molecule-3 on
Platelets: A New Member of Immunoglobulin Superfamily.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                         310 AA
                                                                                                                                                           POTENTIAL
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EMBL; AK074769; BAC11195.1;
EMBL; AK075309; BAC111538.1;
INTERPEO; IPR007110; IG-like.
InterPeo; IPR003006; IG-MHC.
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PROSITE, PS50835, IG LIKE; 2.
Hypothetical protein; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JAM-2 OR JAM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unctions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                      TRRDSALYRCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGRMATLHCQESE 164
                                                                                                                                                                                             TRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKE 137
                                                                                                                                                                                                                                                                                          GNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNS 197
                                                                                                                                                                                                                                                                                                                   198 VGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE--TSFQ- 252
                                                                                                                                                                                                                                                                                                                                                                                                                  225 AGSARCEEQEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKN 284
                                                                                                 21 YQEAILAC-KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 TRSDAGKYRCEVSAPSEQGONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                               Gaps
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heart and identification of a candidate gene, JAM3, expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 YQEAILAC-KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
       DB 4; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 355;
                                                      97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiogenesis.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ416101; CAC94776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN 76 355 JUNCTION ADHESION MOLECULE SEQUENCE 355 AA; 39602 MM; 8B1577DEA7B1D4F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Junction adhesion molecule 3.
    33.7%; Score 477.5; DB 4
38.0%; Pred. No. 2.8e-36;
ive 57; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.7%; Score 477.5; DB 4
38.0%; Pred. No. 3.4e-36;
iive 57; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 PGKPDGVNYIRTDEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00408; IGC2; 1.
Query Match
Best Local Similarity 38.0%
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:15532; JAM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin domain.
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9; Mismatches

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                                    CTRAINGESTREE, FROM N. N. STREE EMBLYONIC stem cells;

NEDLINE=2108660; PubMed=11217851;

NEDLINE=2108660; PubMed=11217851;

NEDLINE=2108660; PubMed=11217851;

NEDLINE=2108660; PubMed=11217851;

NATARAWA T., ABIDARAWA T., SAMEMAWA T., SAILO R., SAILO T., ORZAZAH, Y., GOJODOTI T., BOND H., KANDAWA T., SAILO R., SAILO T., ORZAZAH, Y., GOJODOTI T., BOND H., KANDAWA T., SAILO R., SAILO T., SAILO R., ABIDATMER M., BATABLOW S., CABAVANT T., SAILO R., ABIDAMAMA T., SAILO R., SAILO R., MATSUDA H., ASHDATMER M., PEGALO G., QUACKENDUBH J., RUBHI P., LEWIS S., MATSUD Y., NIKAMOD T., PEGALO G., QUACKENDUBH J., SAKAMI L.M., STAUDH F., SULUKI R., TOMITA M., WAGNET L., WABHIO T., BARAI R., ORIGO T., FUTUNO M., AONO H., Baldarelli R., Barsh G., BIRE J., BOFFFEIL D., BOJUNGA N., CARNING P., RAIDOLDI M., ABLODOR P., HILL D., HOFMANN M., CANING P., WASHIO T., SAKAMOTO N., LYONG P., MATCHION M., ROACHOR P., KING B., RINGWALD M., ROACHORE P., SAKAMOTO N., SASAKI H., SATO K., SCHOENDACH C., SEYA T., Shibata Y., Storch K.-F., SULUKI H., TOYO-OKA K., WANG K.H., WEIZ C., WHITTEKET C., WILLMING L., ARASABRIZAKI Y., ABASHAIZAKI Y., KAWAJI H., KOHTSUKI S., ARASABRIZAKI Y., ABASHAIZAKI Y., KAWAJI H., KOHTSUKI S., ARASABRIZAKI Y., ABASHAIZAKI Y., KAWAJI H., KOHTSUKI S., ABASHAIZAKI Y., KAWAJI H., KAMANDA Y., KAMANDA Y., KAMANDA Y., KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BMBL; AK010826; BAB27208.1;
EMBL; AK01082; BAC32219.1; -.
          138 GNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCBARNS
                                                                                         198 VGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE--TSFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4740167M24Rik protein (Junction cell adhesion molecule 2).
JCAM2 OR 2410167M24RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGL:125555; IG.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig.-like.
InterPro; IPR003006; Ig. MHC.
Ffam; PF00047; Ig; 1.
SMART; SM00409; IG; 1.
SMART; PS0035; IG LIKE; 1.
RROSITE; PS0835; IG LIKE; 1.
SROMENCE 181 AA; Z0330 MM; 603B6114FBB11AEB CRC64;
                                                                                                                                                                                                                                                                                                                    181 AA
                                                                                                                                                                                                 330 PGKPDGVNYIRTDEEGDFRHKSSFVI 355
                                                                                                                                                                            --KSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1933820; Jcam2.
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STRAIN=C57BL/6J;
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DB 11; Length 181;

31.8%; Score 451.5; DB 1.80.0%; Pred. No. 3.6e-34;

Best Local Similarity

Query Match

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59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQS-INSSYTMNTKTGTLQFNTVSK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 LDTGEYSCEARNSVG-YRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKG 243
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 21584683; PubMed=12466851;

The FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

Than41y21s of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

In Nature 420:563-573(2002).

In Rembi, BC021896, AA4121876.1; -.

R EMBL, AK031574; BAC28169.1; -.

R InterPro; IPR007110, Ig-like.

R InterPro; IPR0031006; Ig-MHC.

R InterPro; IPR003406; Ig-W.

R Pfam; PF00047; ig; 2.

SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                     23 YHKANGFSASKDHRQEVIVIEFQEAILACKTPKKTTSSRLEWKKVGGGUSLVYYQQALQG
                                           1 YHKAYGFSAPKD-QQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 YTAQSDVQVPE----NESIKLTCTYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 FSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRA
Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                           12;
                                                                                                                                   60 DFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVL
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12; Indels
                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Junction cell adhesion molecule)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00406; ĬĠv; 1.
PROSITR; PS50835; IG LIKE; 2.
Wypothetical protein.
SEQUENCE 300 AA; 32423 MW; 3CE561E8FF3B97EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 YF---SKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 410; DB 11;
Pred. No. 5.4e-30;
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88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 35.9:
es 99; Conservative
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                            RESULT 11
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InterPro; IPP003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Immunoglobulin domain.
SEQUENCE 259 AA; 28122 MW; F
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Q9JKD5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 IGNRAVLTCSEHDGSPPSEXSWFKDGVPMLTADAKKTRAFINSSYTIDPKSGDLVFDPVS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 KLDTGEYSCEARNSVG-YRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AEMIDFNIRIKUVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 GFSSP------RVEWKFVQGSTTALVCYNNQITVPYADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 SGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQS-TNSSYTMNTKTGTLQFNTVS
                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 409.5; DB 11; Length 300; Pred. No. 6e-30; A9; Mismatches 98; Indels 35;
                                                                                                                                                                                                                                                                                                                                                      Assima H., Kojima I.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR78598, AR782500.1;
InterPro; IRR0031010; Ig-like.
InterPro; IRR003306; Ig_MRC.
InterPro; IRR003306; Ig_V.
Pfam; PF00047; ig; 2.
SNART; SM0046; IGv.
PROSITE; PS50835; IG_LIKE; 2.
SROENCE 300 AA; 32369 MW; 45AE362A96158BFA CRC64;
                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Junctional adhesion molecule JAM.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Junction adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 GYF---SKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 AA
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                                           PRELIMINARY;
                                                                                                                                                                                                        Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague Dawley;
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Best Local Similarity
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                                                                                                                                                                           29 SCAYSGFSSPRAASYEDRUTFLPTGITFKSVTREDTGTYTCMVF--EEGGNSYGEVKVKL
                                                                                                                                                                                                                                               107 EVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNS
                                                                                                                                              47 SVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 LILGILVFGIWFAYSRGHFDRT---KKGTSSKKVIYSQPSARSEGEFKQTSSFLV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 LVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSOS-TNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 ALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKA----TTMSENDFKHTKSFII 276
                                                                                                11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 173;
                                            Query Match 27.8%; Score 393.5; DB 4; Length 259; Best Local Similarity 36.9%; Pred. No. 1.5e-28; Matches 87; Conservative 41; Mismatches 97; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kirsch T., Wellner M., Haller H., Lippoldt A.;
«Cloning of the rat junctional adhesion molecule (JAM).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF241261; AAF61729.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FE38521A911582D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 AA; 18706 MW; 3EE3ECDFA5AFB8B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ©9JKDS;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Last sequence L-MAR-2003 (TrEMBLrel. 23, Last annotation Junctional adhesion molecule (Fragment) Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig c2.
InterPro; IPR003006; Ig MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00047; 1g; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 1.
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45; Mismatches 101; Indels 90; Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 ITAATSPGNASITISNMQPSDTGSYTCEVFSPQDDAGQS--QKSVIVNVLVKPSKPFCKI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 PSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 NTVSKLDTGEYSCEARNSVGYRRCPGKRMQVD-----DLNI--SGIIAAVVVVALVISV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 CGLGVCYAORKGYFSKE----TSFOKSNSSK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 YGFSAPKDOQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGDFKNR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 WSFYSAKESQLHTIYYYSE------GEFKDR 88
                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vainio O.;
"ChT1, a new IgSF member inhibits thymocyte differentiation at the double positive stage.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y14064; CAA74391.1;
HSSP; P06907; INEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=H.B19; TISSUE=Thymus;
Katevno K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 15.9%; Score 225; DB 13; Length 335; Local Similarity 24.1%; Pred. No. 1.2e-12; Nes 75; Conservative 45; Mismatches 101: Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIĞNAL 1 21 POTENTIAL.
CHAIN 22 335 CHTI THYMOCYTE ANTIGEN.
SEQUENCE 335 AA; 36509 MW; AA6159598079B418 CRC64;
                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
CHT1 thymocyte antigen precursor.
                                                                             335 AA
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_W.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus.
NCBI_TaxID=9031;
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RESULT 15
109PWR4
AC 09PWR
AC 09PWR
DT 01-MA
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COC Gallu
COC Ga
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Search completed: December 9, 2003, 17:13:00 Job time : 29.8118 secs

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Human secreted pro
Human gene 25 enco
Human secreted pro
Human secreted pro
Human gene 162 enc
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Human junctional a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1992.DAT:*
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| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1995.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                         276
1 YHKAYGFSAPKDQQVVTAVX.....SSKATTMSENDFKHTKSFII 276
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                           US-09-852-797-76_COPY_23_298
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                                                                                                                                    protein search, using sw model
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AAU00512
ABP61801
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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Maximum DB
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AAO16452 AAY08060 AAY23324 AAY13354	AAB3421 AAB24401 AAY70668 AAU12339 AAU0222	AAB50904 AAB53081 ABU69632 ABU71455 ABU71901	ABU07738 ABU66737 ABU67013 ABU67355 ABU59818 ABU64509 ABU54357	AAM1947 AAB70500 AAB7277 AAM33693 AAM3161 ABG22341 ABG22339 ABG22339
2002	222222	2 2 2 2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4	44444444	2222222222
298 312 312	312 312 312 312 313	312 312 312 312	312 312 312 312 312	222 215 213 303 107 140 69 66
87.0 83.3 83.3	1 M M M M M	88 88 88 88 88 88 88 88 88 88 88 88 88		20.1 38.1 38.1 38.1 38.1 18.5
2222 2330 2300 230	00000000000000000000000000000000000000	5330 5330 5330 5330	00000000000000000000000000000000000000	222 215 183 107 107 73 69 51
10 11 13 13	113 114 114 118	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	33088788 3308878	, ш ш ш ш ш ш д и ш ч ш ш ш ш ш д

ALIGNMENTS

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Human; secreted protein; fusion protein; gene therapy, protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; sathma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                        Human secreted protein encoded by gene 25 clone HTEEB42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
AAW75220 standard; Protein; 298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= unknown
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97US-0040710.
97US-0040762.
97US-0048100.
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                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
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14-MAR-1997;
30-MAY-1997;
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                                                                                                              29-JAN-1999
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                                                       AAW75220;
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11-MAY-2001; 2001US-0852659.
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Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PISCHER C L.
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SOPPET D R.
GENTZ R L.
WEI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-598780/64
                                                                                                                                                                                                                                                                                                                                                                                               RUBEN S M.
ROSEN C A.
                                                                                                                                                                                                                                                             Misc-difference 58
                                                                                                                                                                                                                            Misc-difference 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD44660.
                                                                                                                                                                                                                                                                                                                                                                                                                               ZENG Z.
KYAW H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic use
                                                                                                                                                                                                                                                                                                        US2002077287-A1
                                                                                                                                                                                                                                                                                                                                                                          11-SEP-1998;
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                              20-JUN-2002
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Ferrie AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM,
                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FISC/)
(LIHH/)
                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                               (RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                           ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                (ZENG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                           (KYAW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (/ddos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEIX/)
 This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic acid sequences. AAV4286-V43425, amino acid sequences AAV75196-W75235) which are useful for preventing, treating on an enclorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 28 polymucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRIGSGSTNSSYTMNTKTGTLQFN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLBVLVAPAVPSCEVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                   Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                             99.3%; Score 274; DB 19; Length 298; 100.0%; Pred. No. 1.2e-260; tive 0; Mismatches 0; Indele (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
                                                                                         Greene JM, Kyaw H;
Ruben SM, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                Claim 1; Page 168-169; 201pp; English.
                                                                                        Fischer CL, Gentz RL, ', Moore PA, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                   (see AAV34286 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE26983 standard; Protein; 298
97US-0048189.
97US-0048357.
97US-0050934.
97US-0048970.
                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                             97US-0057765.
                                                                                                             Young PE, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 276; Conservative
                                                                                                                                    WPI; 1998-520811/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       298 AA;
                                                                                                                                               N-PSDB; AAV34310.
                                                                                                    Li Y,
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
                                             05-SEP-1997;
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                                   06-JUN-1997
                                                                                        Ferrie AM,
                                                                                                . H,
. YF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
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Best Local
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ID AAE2
XX AAC AAE7
XX I3-1
XX I3-1
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whuman; immundeficiancy. X-liked agammaglobulineania; septic shock; autochigamme disorder; rhumacoid arthritis; mantiple selectoris; cancer; My read-selection disorder; actument disorder; returned the mantiple selection disorder; actument disorder; mantiple disorder; actument disorder; actument disorder; mantiple di
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/note= "Encoded by TSC"

US2002076756-A1 20-JUN-2002 11-MAY-2001; 2001US-0853161. 02-FEB-2001; 2001US-265583P.

by GWG"

/label= Unknown /note= "Encoded l Misc-difference 58

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including septic shock, sepsis, reperfusion injury, inflammatory bowel disease, and allergy, dascroint respiratory sequences of disease, crohn's disease, allergy, dascrointestinal disorders e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory bowel disease, cancers e.g., gastric, ovarian, lung, invertee of disorders e.g., gastric, ovarian, lung, liver bladder and breast), central nervous system (CNS) disorders e.g., schaemic brain injury and/or stroke, neurodegenerative disorders e.g., retarkinson's disease and Alzheimer's disease, AIDS-related dementia and prion disease, cardiovascular disorders e.g., mpocarditis, arrhythmias, pancreatitis, sarcoidosis and allogenic transplant rejection, blood-related disorder (thrombosis, arterial thrombosis, atherosclerosis), should cancer thrombosis, arterial thrombosis, atherosclerosis), should cancer to sorders e.g. thinitis, should cancers, endorine disorders e.g., hyperthyroidism, Addison's disease, hyperpluitarism, infectious diseases and reproductive system cancers, all ergoreders e.g., actual disorders e.g., hyperthyroidism, Addison's disease, hyperpluitarism, infectious diseases and reproductive system cancers, all ergoreders e.g., actual disorders e.g., actual disorders e.g., actual disorders e.g., hyperthyroidism, human e.g., e.g., endometriosis The present sequence represents a human e.g., e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.2e-260;
Matches 276; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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LI H. SOPPET D R. GENTZ R L.

GENT/ MOOR/

PISCHER C L

(KYAW/) LIHH/ (Vados)

ZENG Z. KYAW H.

RUBEN S M. ROSEN C A. LI Y.

ROSE/

WEI Y.
MOORE P A.
YOUNG P E.
GREENE J M.
FERRIE A M.

YOUN/

(GREE/) (FERR/)

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Human; secreted protein; autoimmune disease; hyperproliferative disorder rheumatoid arthritis; neoplasm; cerebrovascular disorder; anglogenesis; cerebral ischaemia; cardiovascular disorder; nervous system disorder; cardiac arrest; Alzheimer's disease; ocular disorder; wound healing; infection; corneal infection; skin aging; food additive; preservative; tissue regeneration; immunosuppressive; antiproliferative; cycostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antipacterial; virucide; fungicide; ophthalmological; gene therapy;
                                                                                                                                         Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
                               AAE27121 standard; Protein; 298 AA
                                                                                                       (first entry)
                                                                                                       13-DEC-2002
                                                                                                                                                                                                                                                                                                                     vulnerary.
                                                                    AAE27121;
RESULT 3
                AAE2712
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/note= "Mature human secreted protein"

/label= Signal_peptide 23..298 cocation/Qualifiers

> Protein Peptide

Homo sapiens

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AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC AAE27134 ASE27137 represent the proteins they encode.
AAE27138 AAE27134 represent human secreted protein fragments. The genes
and their corresponding secreted proteins are useful for preventing,
treating or ameliorating medical conditions, e.g., by protein or gene
therapy. Secreted protein sequences of the invention are useful for the
diagnosis or treatment of disorders auchimmune diseases (e.g.
thermatoid arbritis), hyperproliferative disorders (e.g. neoplasms of
the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
angiogenesis), cardiovascular disorders (e.g. cerebral ischaemia,
cc angiogenesis), cardiovascular disorders (e.g. cerebral ischaemia,
system disorders (e.g. Alzheimer's disease), infections caused by fungi,
bacteria and viruses and ocular disorders (e.g. corneal infection). The
polypeptides can also be used to aid wound healing and epithelial cell
cpolypeptides can also be used to aid wound healing and epithelial cell
cpolypeptides can also be used to aid wound healing and epithelial cell
cpolypeptides and in chemotaxis. They can also be used as food
additives or preservative to increase or decrease storage capabilities,
cf fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
content, and other nutritional components. The present sequence represents a human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.3%; Score 274; DB 23; Length 298; 100.0%; Pred. No. 1.2e-260;
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ses 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Matches
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New nucleic acid molecules encoding 28 human secreted proteins, useful for diagnosing, preventing, treating or ameliorating medical conditions and as food additives or preservatives

Claim 11; Page 186-187; 209pp; English.

Li Y, Zeng Z, Kyaw H, Fischer CL, Li N Wei Y, Moore PA, Young PE, Greene JM;

Gentz RL,

Soppet DR, Ferrie AM; Š

Rosen CA,

Ruben

WPI; 2002-574454/61.

N-PSDB; AAD44878

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ABU64994 standard; Protein; 298
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97US-040762P.
97US-048100P.
97US-048189P.
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                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Watches 276; Conservative
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                                                                                                                                                                                          298 AA;
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14-MAR-1997;
30-MAY-1997;
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                                                                     metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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(ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The

proteins and their coding sequences are useful for the preparation of a

diagnostic or pharmaceutical composition for diagnosing or treating a

cardiovascular disorder (e.g., arxhythmia, tachycardia, cardiac arrest,

cardiovascular disorders, muscular disorders, neural disorders,

immune system disorders, pulmonary disorders, renal disorders,

cardiovascular disorders, pulmonary disorders, renal disorders,

cyconary arteriosclercs; pulmonary disorders, renal disorders,

cyconiferative disorders and/or cancerous disease and conditions, for

proliferative disorders and/or cancerous disease and conditions, for

cyconiferation for treating thrombosis and arteriosclerosis, for treating or

confection, for treating thrombosis and arteriosclerosis, for treating or

confection, for treating thrombosis and arteriosclerosis or

confection, for treating thrombosis and arteriosclerosis, for treating or

confection, for treating thrombosis and arteriosclerosis, for treating or

confection, for treating thrombosis and arteriosclerosis or

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confection, for treating thrombosis and arteriosclerosis or

confection, for treating thrombosis and arterio
                                                                                                                    SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
                                                                                                                                                              202
                                                                                                                                                                                                             TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                                                                                                                                                                                      Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
                                                 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                               SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFN
                      FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia -
                                                                                                                                                                                                                                                                                                                               RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein, SEQ ID 817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR47926 standard; Protein; 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001; 2001US-277340P.
19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-129429/12.
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; rheumatoid arthritis; diabetes mellitus; haematopoietic disorder; inflammatory condition; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; lschaemic brain injury; neurodegenerative disorder; Parkinson's disease; blood-related disorder; thrombosis; atherosclerosis; blood-related disorder; autre glomerulonephritis; Addison's disease; endocrine disorder; autre glomerulonephritis; Addison's disease; endocrine disorder; liver disease; reproductive system disorder; wound repair; angiogenesis; lymphatic disorder; vaccine; wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
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organs before transplantation or for supporting cell culture of prime tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or
                                                                                                                                            Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                   Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                          Score 274; DB 24; I Pred. No. 1.2e-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
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100.0%; Pred. No. ...
0; Mismatches
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The invention relates to an isolated polypeptide comprising an amino acid compressed at least 95% identical to sequence of 28 human secreted form, proteins, their fragment, polypeptide domain, epitope, secreted form, ariant, allelic variant, or psecies homologue, or the encoded sequence included in ATCC 97921 and 97922. Also included are the encoding mucleic acids, recombinant vectors, host cells, antibodies, and genes. The proteins and mucleic acids are useful for diagnosing, preventing, treating, prognosing or ameliorating a medical condition e.g. immunodeficiencies, severe combined immunodeficies, demarticis, cancers (e.g. seximan and allarey), gastroinnessie, chork disease, concertication seystem (CNS) disorders (e.g. septic shock, traumant chorse severe complications, inflammatory conders, lateral and cardiopulmonary company mylory, central nervous system (CNS) disorders (e.g. ischaese, AnDe-related disorders (e.g. gastric, ovarian, lung, bladder, liver and cardiopulmonary complement and sease, and cardiopulmonary complements of sease, and cardiopulmonary complements of seases, and cardiopulmonary complement disorders (e.g. demerticis, sarcoidosis, dermarticis, and prior disease, reparaticis, sarcoidosis, dermarticis, and prior disorders, renal disorders (e.g. demerticis, complement disorders (e.g. demerticis, complement disorders (e.g. dedmerticis), infectious disease, complement disorders (e.g. demertici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human secreted polypeptides and polynucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                              Zeng Z, Kyaw H, Fischer CL, Li
Moore PA, Young PE, Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 186; 209pp; English
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Wei Y,
97US-050934P.
97US-048970P.
97US-057765P.
97US-060368P.
1201US-265881P.
98WO-US04858.
                                                                                                                                                                                                                                                                                                                                                                                       CA,
                                                                                                                                                                                   ZENG Z.
KYAW H.
FISCHER C L.
LI H.
                                                                                                                                                                                                                                                       SOPPET D R. GENTZ R L.
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                                                                                                                                                                                                                                                                                                         MOORE P A.
YOUNG P E.
                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA
Gentz F
                                                                                                                                                                                                                                                                                                                                           GREENE J M.
FERRIE A M.
                                                                                                                                     RUBEN S I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABX96990
                                                                   02-FEB-2001;
                                                                                                   11-SEP-1998;
                                                                                     12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
Soppet DR,
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Ferrie AM;
                                                                                                                                                                                                                                                                                                                       (YOUN/)
(GREE/)
(FERR/)
                                                                                                                                                                                   (ZENG/)
(KYAW/)
(FISC/)
(LIHH/)
                                                                                                                                                       (ROSE/)
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                                                                                                                                                                                                                                                                                                    SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
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                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; biliary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cycostatic; gene therapy; antlinflammatory; immunosuppressive; vulnerary; chromosome 21q21.2.
                                                                                                                                                                                           23 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                          83 FKNRAEMIDENIRIKNVTRSDAGKYRCEVSAPSEQQQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                                                                                      1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                                                                                             TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ
                                                                                                                                            Gaps
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capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins also useful for identifying binding partners. The present sequence represents a secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene 162 encoded secreted protein HTEEB42, SEQ ID NO:461.
                                                                                                           Length 298;
                                                                                                                                          Indels
                                                                                                             Score 274; DB 24; I
Pred. No. 1.2e-260;
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                                                                                                                                                                                                                                                                                                                                                                                                                           241 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
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                                                                                                                    100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR00172 standard; Protein; 298
                                                                                                             99.34;
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-2002; 2002WO-US08276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                          Best Local Similarity 100. Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME
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                                                                              298 AA;
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                                                                                                                                                                                                                                                                                                  121
                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR00172;
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ABZ71190-ABZ71478 represent CDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, and recombinant to exercise and host cells comprising a nucleic acid of the invention. The secreted proteins in uncleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, coesophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The cereted proteins and their nucleic acids may also be used in the creatment of immune disorders, inflammation, infection, chromosome companing, in gene therapy, for identifying individuals from minute markers. The present sequence represents a human secreted protein of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIJAAVVVVALVISVCGLGVCYAQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 YHKAYGFSAPKDQQVVTAVXYQEAIIACKTPKKTVXSRLEWKKGRSVSFVYYQQTLQGD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
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                                                                                                                                                                                                                                                                                                                                                                                                             99.3%; Score 274; DB 24; Length 298; 100.0%; Pred. No. 1.2e-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW85457 standard; Protein; 298
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Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                              298 AA;
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                                                                                                                                                                                                                                                                                                                                            invention.
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98WO-US05653

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The present sequence represents a secreted protein. The polynucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating activity, tissue growth activity, activin/inhibin activity, chemokinetic activity, haematopoiesis regulating chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, and thrombolytic activity, invasion suppressor, activity, and tumour inhibition activity (no data is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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                                                                                                                                                                                                                                                                                                                                                                                           human foetal brain, adult brain, foetal kidney, placenta or adult pineal gland cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding secreted human proteins - derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          given in the specification to support these activities). The polynucleotide is also stated to be useful for gene therapy.
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                                                                                                                                                                                  McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3e-227
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                                                                                                                                                                               Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 73-74; 113pp; English.
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                            98US-0044466.
97US-0822167.
                                                                                                                      (GEMY ) GENETICS INST INC.
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les 240; Conserv
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                            19-MAR-1998;
                                                         21-MAR-1997;
                                                                                                                                                                               Agostino MJ,
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80 X C C C C C C C C C X R X L L L X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B
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The sequence represents a human junctional adhesion molecule 2 (JAM2). The polynucleotide encoding the polypeptide is useful for recombinant production of JAM-2 protein, which in turn is useful for the production of antibodies. The antibodies may be used for probing cellular localisation and/or expression of JAM2 in tissues under normal and disease states, for immunoprecipitating JAM2 protein from cells and/or stroke tissues to determine whether it is modified by glycosylation and phosphorylation, and for determining JAM2 function. The antibodies inhibit interaction of JAM2 with inflammatory cells or influences their paracellular migration, and is therefore useful for alleviating inflammatory diseases such as arthritis, asthm, rheumatoid arthritis, inflammatory bowel disease and Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding human junctional adhesion protein useful for producing antibodies that are suitable for therapeutic purposes
               /note= "Possible signal peptide #1"
                                               "Possible signal peptide #2"
                                                                               "Possible mature JAM2 #1"
                                                                                           ..298
ote= "Possible mature JAM2 #2"
                                                                                                                                             /note= "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                       Cunningham S, Trindad Arrate Barros M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 46-47; 51pp; English.
                                                                                                                                                                                                                                                                                                         (TEXA-) TEXAS BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                            23-AUG-2000; 2000WO-US23158
                                                                                                             /note= "P
237..254
                                                                21..298
                                                  /note=
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                                Peptide
                                                                Protein
                                                                                              Protein
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QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156 PRIGSOSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS Gaps ö 87.0%; Score 240; DB 22; Length 298; 100.0%; Pred. No. 3e-227; ive 0; Mismatches 0; Indels (Best Local Similarity 100. Matches 240; Conservative 119 179 217 37 59 97 157 239 qq 셤 요 ð ò ò ò

ABP61801

RESULT 9
ABP61801
ID ABP6
XX
AC ABP6
XX

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The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary deoxyribonucleic caid (CDNA) inserts (II), where the protein is substantially free from acid comblements. (I) are useful for preventingly treatment or other mammalian proteins. (I) are useful for preventing, treatment or meallorating a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activin or inhibin-related activities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace colls damaged by illness, autoimmune disease, accidental damage or regeneration of nerve and brain tissue mid is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as altorial soll peripheral nervous system diseases and neuropathies, contact activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia con lymphoid cell disorders, platelet disorders such as thrombocytopaenia con lymphoid cell disorders, platelet disorders such as thrombocytopaenia con lymphoid cell disorders, platelet disorders such as thrombocytopaenia con lymphoid cell disorders, platelet disorders such as thrombocytopaenia con lymphoid cell disorders, platelet disorders such as thrombocytopaenia con treating osteoporosis, cartilage, tendon, ligament and/or nerve con lymphoid cell disorders, platelet disorders such as thrombocytopaenia con treating osteoporosis, cartilage, tendon, ligament and/or nerve con periodomial disease. (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperturiation in warious tissues, various immune deficiencies and disorders including autoimmune disorders e.g. multiple sclerosis, reperturiat
Claim 54; Page 116-117; 284pp; English.
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Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis

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Collins-Racie LA,

Treacy M, McCoy JM,

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Merberg

Jacobs K,

WPI; 2002-582343/62

N-PSDB; ABQ92017

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Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antianflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulicer; fungicide; antidibecic; antiaschmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.
                                                                                                                                                                                                                                                                                                      LaVallie ER, C
                   Human polypeptide SEQ ID NO 155
                                                                                                                                                                                          22-DEC-2000; 2000US-0745763.
                                                                                                                                                                                                             98US-0040963
04-OCT-2002 (first entry)
                                                                                                                                                                                                                                                          COLLINS-RACIE L A.
                                                                                                                                                                                                                              JACOBS K.
MCCOY J M.
LAVALLIE E R.
                                                                                                                                                                                                                                                                                             SPAULDING V.
                                                                                                                                                                                                                                                                          MERBERG D.
                                                                                                                                                                                                                                                                                    TREACY M.
                                                                                                                                                       US2002065394-A1.
                                                                                                                                                                                                             18-MAR-1998;
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                                                                                                                                       Homo sapiens.
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(MCCO/)
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(first entry)
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21-NOV-1997;
24-NOV-1997;
04-JUN-1998;
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such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
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                                                                                                                                                                              Gaps
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polypeptide, useful for treating an immune system disorder such as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Extracellular domain; Specifically claimed
                                                                                                                                                                             ö
                                                                                                                                            Length 298;
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                                                                                                                                          Score 240; DB 23;
Pred. No. 3e-227;
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                                                                                                                             87.0%; Scor.
100.0%; Pred. No. sc.
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/label= Signal_peptide
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05-FEB-2002; 2002US-354345P.
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/note= "]
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Best Local Similarity
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N-PSDB; AAL51599.
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                                                                                                       298 AA;
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                                                                                                                                           The invention comprises the DNA and protein sequences of the extracellular region of human junctional adhesion molecules (huJAM). The extracellular huJAM DNA and protein sequences are useful in the treatment of: immune system disorders (e.g. immune deficiency); autoimmune disorders, inflammatory disorders, cancer; wound healing; or a cardiovascular disease. The present amino acid sequence represents the full-length membrane-bound huJAM2 protein.
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immune deficiency or an inflammatory disorder, cancer, wound healing, or a cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 240; DB 24;
100.0%; Pred. No. 3e-227;
iive 0; Mismatches 0;
                                                                                       Disclosure, Fig 1; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0%; P. Matches 240; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 312
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97US-0063550.
97US-0065186.
97US-0066364.
97US-0066770.
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AAY23324 standard; Protein; 312 AA.

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This introlled describes a movel PRO25 polypeptide (1), its agonist trom a carrier or excipient), a novel PRO25 polypeptide (1), its agonist or antagonist, or their fragments, for modulating; (i) infiltration of inflammatory calls into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects (i)-(iii). The products of the invention have anti-inflammatory, continuorismume and anti-diabetic activity. (i), and its (ant) agonists anti-autoimmune and anti-diabetic activity. (i), and its (ant) agonists and their fragments, are used to treat immune related diseases, particularly T cell-mediated diseases. The diseases treated include particularly T cell-mediated diseases. The diseases treated include created include architis, spondyloarthropathies, systemic sclerosis (scleroderma). Garbritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, putonimune chemistry and idiopathic immune pancytopenia (idiopathic thrombocytopenia (idiopathic thrombocytopenia), thyroiditis, atrophic cryptopathic inflammatory and interstitial nephritis), multiple sclerosis, cidiopathic demyelinating polymeuropathy, duillain-Barre syndrome, chronic chronic active hepatitis, primary biliary cirrhosis, granulomatous chronic active hepatitis, primary biliary cirrhosis, granulomatous chronic active hepatitis, primary biliary cirrhosis, granulomatous con whitned or inflammatory benefitie, inflammatory benefitie, and sclerosing cholmagitie, inflammatory bowel disease con whitned or inflammatory contines cronn's disease, and disease cronn's disease and disease cronn's each of memory and sclerosing chimics and sclerosing chimics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel composition containing (apart from a
                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition containing novel polypeptide PRO245, its agonist or
                                                                                                                            Wood WI;
                                                                                                                            Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 2; 177pp; English.
                                                                                                                            Gurney AL,
(GETH ) GENENTECH INC
                                                                                                               Fong S, Goddard A,
                                                                                                                                                                                                                                            WPI; 1999-229499/19
N-PSDB; AAX37664.
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Matches 230; Conservative Local Similarity 312 AA; Sequence 59 Query Match 셤 8 ሯ ö 59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156 216 96 37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 119 ONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS Gaps **;** 0 288 83.3%; Score 230; DB 20; Length 312; GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 0; Indela 2.1e-217; 100.0%; Pred. No. 2.1 ive 0; Mismatches Best Local Similarity Lou. Matches 230; Conservative 312 AA;

97

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217 239

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AAY23324

Seguence Query Match ö

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PRO245. The methods and compositions of the invention are useful for the treatment and diagnosis of inflammatory disease and tumours in mammals. Such inflammatory disease and tumours in mammals. Such inflammatory disease and tumours in mammals. Such inflammatory disease and tumours in mammals. Systemic lupus erythematosis, rheumatory bavel disease.

C systemic lupus erythematosis, rheumatoris polymyositis, polymyositis, polymyositis, polymyositis, polymyositis, polymyositis, polymyositis, polymyositis, commune hamolytic arthritis, sarcoidosis, autoimmune hemolytic anemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria, antommune thrombocytopenia, phyroiditis, Grave's disease, immune-mediated thrombocytopenia, phyroiditis, Grave's disease, immune-mediated thrombocytopenia, phyroiditis, Grave's disease, corpyroiditis, diabetes mellitus, immune-mediated renal disease, cy phyroiditis, tubulointerstitial nephritis, demyelinating diseases, infectious hepatitis at of the central and peripheral nervous systems such as multiple sclerosis, cof the central and peripheral nervous systems such as multiple sclerosis, didopathic polymeuropathy, diseases, infectious demyelinating corporation, inflammatory and fibrotic lung diseases, inflammatory and fibrotic lung diseases allergic diseases of the lung such as eosinophilic pneumonias, contamparion asserviated diseases and hypersensitivity pneumonias, rannershantarion asserviated diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification describes A33 related antigens PRO301, PRO362 and
                                                                                                                                                       A33 related antigen; PRO301; PRO362; PRO245; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplantation associated diseases disease. The present sequence represents PRO245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gurney AL, Napier MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigens PRO301, PRO362 and PRO245 related to A33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fong S, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 11; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                98WO-US24855
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                                                                                                                A33 related antigen PRO245.
                                                                          (first entry)
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Tumaa D, Wood WI
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                                                                                                                                                                                                               Homo sapiens.
                                                                          02-SEP-1999
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                                                                                                                                                                                                                                                                                                                              20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1997;
20-MAR-1998;
                                                                                                                                                                                                                                                                                        03-JUN-1999
                                    AAY23324;
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RESULT 14
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          PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216
                                                                                                                                                              Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvilus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alcheimer's disease; Alcheimer's fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 266
                                          Amino acid sequence of protein PRO245.
                                                                                          AAY13354 standard; Protein; 312
                                                                                                                                                                                                                                                                                                              9708-0059113
9708-0059115
9708-0059115
9708-0059117
9708-0059121
9708-0059121
9708-0059184
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97US-0063564.
97US-0063564.
97US-0063704.
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97US-0063734.
97US-0064215.
97US-0063735.
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                                                                                                                             (first entry)
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                                                                                                                                                                                                                                     Homo sapiens
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28-OCT-1997
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                                                                                                             AAY13354;
157
                179
                                217
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24-0CT-19
24-0CT-19
24-0CT-19
24-0CT-19
24-0CT-19
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27-0CT-19
27-0CT-19
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                                                                           RESULT 13
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The CDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal comecosa and the repair of acute and chronic mucosal lesions

C (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal culceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), concers such as lung squamous cell carcinoma of the vulva and gliomas), corners such as lung squamous cell carcinoma of the vulva and gliomas), corners such as lung squamous cell carcinoma of the used as corners such as lung squamous cell carcinoma of the vulva and gliomas), corners such as lung squamous cell carcinoma of the vulva and gliomas), corners such as lung squamous cell carcinoma of the vulva and gliomas), corners such as lung squamous cell carcinoma of the vulva and gliomas), corners such as lung squamous cells including Parkinson's disease, corners corners of the readment of growth or survival of nerve cells including Parkinson's disease, corners corner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Yuan J;
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                                                                                                                                                                                                                                                                                                                                                                   Wood WI,
                                                                                                                                                                                                                                                                                                                                                                      Gurney AL, Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 24; 320pp; English
97US-0064103.
97US-0064809.
97US-0065186.
97US-0065846.
97US-0065693.
97US-0066120.
97US-0066772.
97US-0066772.
97US-0066771.
97US-0066771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX52225
  31-OCT-1997;
03-NOV-1997;
17-NOV-1997;
17-NOV-1997;
18-NOV-1997;
21-NOV-1997;
21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
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dermatological, antiarthritt; antitheumatic; immunosuppressive; haemostatic; antiarthritt; antidheumatic; immunosuppressive; haemostatic; antithyroid; antidabetic; nootropic; neuroprotective; antiastematic; systemic luque erythematosus; theumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune haemolytic anaemia; diabetes mellitus; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; hepatobiliary disease; Whipple's disease; autoimmune disease; immune—mediated skin disease; allergic disease; immune mediated disease; allergic disease; immune mediated disease; transplantation associated disease;
                                                                                                          Human; immune related disease; diagnosis; antiinflammatory;
                                                                                                                                                                                                                                                                                        graft rejection; graft-versus-host-disease
                                                                                Human PRO245 protein UNQ219 SEQ ID NO:36.
AAB33421 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-USO5028.
99US-0123618.
99US-0123957.
99US-0125775.
99WS-0128849.
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99US-0132371.
99US-0134287.
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99US-0141037.
99US-0144758.
99US-0145698.
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99WO-US20111.
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99WO-US28409
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2000WO-US00376,
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                                                      entry)
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30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
11-FEB-2000;
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20-APR-1999;
28-APR-1999;
04-MAY-1999;
02-JUN-1999;
23-JUN-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                    Homo sapiens
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29-OCT-1999;
29-NOV-1999;
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08-SEP-1999;
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                           AAB33421;
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(GETH) GENENTECH INC

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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and anagonists are useful for treating and disgnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central and peripheral nervous systems, hepatobiliary diseases inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune emdiated skin diseases, allergic disease, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

AACSB37 to AACSB378 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACSB37 to AACSB42 and AACSB42 and AAB33417 represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
                                                                                                                                            Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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  Henzel
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?, Goddard A, Gurney AL, Hebert C, He
in J, Pennica D, Shelton DL, Smith V;
Watanabe CK, Wood WI, Yan M;
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100.0%; Pred. No. 2.1e-217;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                              Claim 33; Fig 16; 309pp; English.
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Matches 230; Conservative
    Baker KP,
                     Kabakoff RC, Lu Y, Pa
Stewart TA, Tumas D,
                                                                                    2000-572271/53.
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N-PSDB; AAC58586.
  Ashkenazi AJ,
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with imappropriate PRO expression such as cardiovascular, endothelial angiogenic disorders in mammals (e.g. atherosclerosis, cancers and angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy. For example, the nucleic acids (NCB) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB2438 to AAB2438 to Expresent nucleotide and protein sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 72; Fig 28; 315pp; English.
                                                                                                                                                                                                             99US-0141037.
99US-0144758.
99US-0145698.
                                                                                         98WO-US25108.
98US-0112850.
99WS-0115554.
99WS-US05028.
99US-0131445.
99US-01314457.
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99WO-US23089
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N-PSDB; AAA77562.
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   WO200032221-A2
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                                                                                                                                    08-MAR-1999)
12-MAR-1999
14-MAY-1999
02-UN-1999
20-UN-1999
20-ULL-1999
26-ULL-1999
01-SIP-1999
08-SIP-1999
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Watanabe CK,
                                                              30-NOV-1999;
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ONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLEN 156 PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216

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179

37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG

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Length 312; 0; Indels

/ Match
Local Similarity 100.0%; Pred. No. 2.1e-217; Les 230; Conservative 0; Mismatches 0;

Query Match Matches

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239 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
217 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 266
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9, 2003, 17:36:04 completed: December ne : 41.3519 secs Search com

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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Gondard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Goddard, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFERENCE: P1216R (US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-103-05
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (58)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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100.0%; Pred. No. 2.5e-261;
iive 0; Mismatches 0; Indels
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EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATCHILING Ver. 2.0
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Best Local Similarity 100.
Matches 276; Conservative
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ORGANISM: Homo sapiens
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Sequence 9, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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276
1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFRENCE: P2003P1.03

CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT FILING DATE: 1998-09-11

EARLIER PILING DATE: 1998-03-12

EARLIER FILING DATE: 1999-03-14

EARLIER FILING DATE: 1997-03-14

EARLIER PILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-03-16

EARLIER FILING DATE: 1997-03-16

EARLIER FILING DATE: 1997-05-30

EARLIER APPLICATION NUMBER: 60/048,100

EARLIER FILING DATE: 1997-05-30
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US-09-254-465A-9
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Maximum DB seq length: 2000000000
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Perfect score:
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Database :

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; PRIOR APPLICATION NUMBER: US 60/078,936; PRIOR FILING DATE: 1998-03-20; PRIOR PILING DATE: 1998-09-17; PRIOR FILING DATE: 1998-09-17; NUMBER: OF SEQ ID NOS: 30; SEQ ID NO 9; LENGTH: 312; TYDE: PRIOR TYDE: PRIOR CRANISM: HOMO Sapiens
US-09-254-465A-9
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Search completed: December 9, 2003, 17:39:14 Job time : 14.4251 secs

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OF INVENTION: 28 Human Secreted Proteins
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CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR PELING DATE: 2001-05-03
PRIOR PELING DATE: 2001-05-03
PRIOR PELING DATE: 1998-09-11
PRIOR PILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-05
PRIOR PILING DATE: 1997-12-19
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Sequence 76, Appl
Sequence 76, Appl
Sequence 38, Appl
Sequence 2, Appl
Sequence 64, Appl
                                                                                                               9, 2003, 17:38:14 ; Search time 33.1777 Seconds (without alignments) 1547.168 Million cell updates/sec
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1 YHKAYGFSAPKDQQVVTAVX.....SSKATTMSENDFKHTKSFII 276
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'(gnz_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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'(gnz_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-852-65A-76
US-09-852-797-76
US-09-79-777-30
US-09-799-777-30
US-10-192-791-2
US-09-909-320-64
US-09-905-291A-64
US-09-905-291A-64
US-09-907-841-64
US-09-907-841-64
US-09-907-841-64
                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters.
                                                                                                                                                                                                                                                                                                                                         684280 seqs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                 US-09-852-797-76_COPY_23_298
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                                                                             OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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19	230	ë.	312	11	07-942-	ø	4	
50	230	e.	312	11	-09-904-859-6	9	4.	
21	230	Ξ.	312	11	-09-909-204-	_	4	• •
22	230	Ξ.	312	11	-09-904-820-6	Sequence 6	4	• •
23	230	Ξ.	312	11	-09-904-786-	Ó	4	• •
24	230	ë.	312	11	-90	Ó	4	
25	230	ë.	312	11	-004-906-60-	Ó	4	·
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27	230	ω.	312	11	-902-90	9	4	·
28	230	έ.	312	11	-09-903-	9	4	·
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30	230	ë.	312	11	-09-904-956-	9	4.	- 14
31	230	Ξ.	312	11	-09-902-736	9	4	14
32	230	~	312	11	-09-907-794-	9	4,	14
33	230	m	312	11	-09-903-943-6	9	4.	14
34	230	m	312	11	-09-904-46	9	Α,	ι н
35	230	~	312	11	-09-907-925-	9	4	14
36	230	~	312	11	-09-902-69	9		, H
37	230	~	312	11	-09-903-5	9	4,	, 14
38	230	~	312	11	-03-302-026-60	9	4	بد
39	230	~	312	11	-09-909-064-6	9	4	بد،
40	230	~	312	11	-09-904-553-	equence 6	4	4 14
41	230	~	312	11	05-381-6	9		, 14
42	230	~	312	11	-905-088-	9		
43	230	~	312	11	-09-907-575-6	9	4	4 14
44	230	~	312	11	-905-075-	equence 6	٠.	, ,
45	230	83.3	312	11	-09-902-759-6	equence 6	4, A	4 14
					ALIGNMENTS			
RESULT 1								
Sequences Patent	ce 76, 1	. 03-033-161-76 Sequence 76, Application US/09853161 Patent No. US20020076756A1	ion US 756Al	860/	53161			
GENERAL	ENERAL INFORMATION APPLICANT: Rosen	MATION: osen et	al.					

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                   FRATURE:

NAME/KEY: SITE

LOCATION: (42)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (58)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-853-161-76
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100.0%; Pred. No. 4.5e-260;
iive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INFORMATION:
FILLE OF INFORMATION:
FILLE OF INFORMATION:
FILLE OF INFORMATION:
FILLE OF INFORMATION:
CURRENT FILLING DATE:
CURRENT FILLING DATE:
CURRENT FILLING DATE:
CON1-05-02
FRIOR PAPLICATION NUMBER: 60/265,583
FRIOR PAPLICATION NUMBER: 60/265,583
FRIOR PAPLICATION NUMBER: PCT/US98/04858
FRIOR PELING DATE: 1998-09-11
FRIOR PELING DATE: 1998-09-12
FRIOR PAPLICATION NUMBER: 60/040,762
FRIOR PAPLICATION NUMBER: 60/040,710
FRIOR PAPLICATION NUMBER: 60/040,710
FRIOR PAPLICATION NUMBER: 60/040,100
FRIOR PAPLICATION NUMBER: 60/048,100
FRIOR FILING DATE: 1997-05-30
FRIOR PAPLICATION NUMBER: 60/048,300
FRIOR FILING DATE: 1997-05-30
FRIOR FILING DATE: 1
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Patent No. US20020077287A1
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 276; Conservative
ORGANISM: Homo sapiens
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FRATURE:
NAME/KEX: 31TB
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                     NAME/KEY: SITE
1 LOCATION: (58)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659A-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 274; DB 9; Length 298;
Pred. No. 4.5e-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR PELLING DATE: 2001-02-02
PRIOR PELLING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-14
PRIOR PILING DATE: 1998-03-14
PRIOR PILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR PILING DATE: 1997-05-30
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99.3%; Score 274; DB
Best Local Similarity 100.0%; Pred. No. 4.5
Matches 276; Conservative 0; Mismatches
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Patent No. US20020172994A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
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                                                                                                                                                                                                                                                                                                                                      Gaps
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Parent No. US20020091244A1

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
Hillman, Jennifer L.

Corley, Nail C.
Guegler, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                         87.0%; Score 240; DB 9; Length 298; 100.0%; Pred. No. 9.2e-227; tive 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOOFWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASISTICATION: -UNKNOWN>
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/09/002,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              TOPOLOGY: linear
NOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-745-763-38
                                        TELEPHONE: (617) 498-8284
TELEPAK: (617) 876-5851
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
        REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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STATE: CALIFORNIA
COUNTRY: USA
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Best Local Similarity 100.0
Matches 240; Conservative
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                                                                                                                                            LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                      ; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-852-797-76
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                                                                                                                                                                                                                                                                                                                                                                      1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
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Treacy, Maurice
Spaulding, Vikit
INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                         Length 298;
                                                                                                                                                                                                                                                                                                                           0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                 99.3%; Score 274; DB 10; I 100.0%; Pred. No. 4.5e-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
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ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                             100.0%; Pred. No.
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APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jacobs, Kenneth
MCCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sprunger, Suzanne A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-745-763-38
i Sequence 38, Application US/09745763
j Patent No. US20020065394A1
j GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 276; Conservative
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SOFTWARE: Patentin Ver.
SEQ ID NO 76
LENGTH: 298
                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                     NAME/KEY: SITE
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APPLICANT: Texas Biotechnology Corporation
TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (J.
FILE REFERENCE: TEX454209430
CURRENT APPLICATION NUMBER: US/10/192,791
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                         59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                                                                                                                                                                                                              QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156
                                                                                                                                                                                                                                                                                                                  PRIGSOSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216
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                                                                                                                                                                                                                                                                                                                                                                                               179 PRIGSQSTNSSYTMATKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMOVDDLNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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                                                                                                                                   n
Similarity 100.0%; Pred. No. 9.2e-227;
10; Conservative 0; Mismatches 0; Indels
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LENGTH: 298 amino acids
TYPE: amino acid
TYPE: alino acid
TYPE: Jinear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/10192791; Publication No. US20030130166A1; GENERAL INFORMATION:
                                                                                                                                                         Best Local Similarity 100.
Matches 240; Conservative
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Matches 240; Conservative
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US-10-139-849-2
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US-10-192-791-2
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Best Local S
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                                                                                                                                                                                                                                                                                                                                              37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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                                                                                                                                                                                                                                                                        Length 298;
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TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN
JUNCTIONAL ADHESION PROTEIN (JAM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N Stetson Avenue, 2 Prudential Plaza,
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/139,849
FILING DATE: 07-May-2002
CLASSIFCATION SUMBER: US/09/643,929
FILING DATE: 23-Aug-2000
ATTORRENT INFORMATION:
                                                                                                                                                                                                                                                                  87.0%; Score 240; DB 9; Length 29
100.0%; Pred. No. 9.2e-227;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 30 US-09-799-777-30
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REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
  TELEPHONE: (650) 855-0555
                                                                        LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/10139849
; Publication No. US20030079238A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Sonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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CLONE: 1704050
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Best Local Similarity 100.04
Matches 240; Conservative
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APPLICANT: Hillan, Kenneth, J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Milliam, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT APPLICATION NUMBER: DCT/US00/0414
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
                           59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                              ONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156
                                                                                                                                            119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
                                                                                                                                                                                                                                                              179 PRLGSQSTNSSYTMNTKTGTLQPNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                                                                                            PRIGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99/23089
FLING DAPR: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DAPE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 64, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                   Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
                                                                            Ferrara, Napoleone
Filvaroff, Ellen
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Mather, Jennie P.
                        Desnoyers, Luc
Eaton, Dan L.
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CRGANISM: Homo sapiens
US-09-909-320-64
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Acids Encoding the Same
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ORGANISM: Homo sapiens
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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100.0%; Pred. No. 6.1e-
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Stewart, Timothy A.
Tumas, Daniel
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Gerber, Hanspeter
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Mather, Jennie P.
Pan, James
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Best Local Similarity 100.0
Matches 230; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-088B-64
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SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
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| TITLE OF LINVENTION: ACLICA SILCULING TO CURRENT APPLICATION NUMBER: US/09/905,291A CURRENT APPLICATION NUMBER: US/09/905,291A CURRENT PILING DATE: 2001-07-12
| PRIOR APPLICATION NUMBER: US 60/143,048 |
| PRIOR FILING DATE: 1999-07-07 |
| PRIOR FILING DATE: 1999-07-07 |
| PRIOR FILING DATE: 1999-07-07 |
| PRIOR APPLICATION NUMBER: US 60/146,222 |
| PRIOR APPLICATION NUMBER: US 60/146,222 |
| PRIOR APPLICATION NUMBER: US 60/146,222 |
| PRIOR PILING DATE: 1999-07-28 |
| PRIOR FILING DATE: 1999-07-13 |
| PRIOR FILING DATE: 1999-09-13 |
| PRIOR FILING DATE: 1999-09-13 |
| PRIOR APPLICATION NUMBER: PCT/US99/21090 |
| PRIOR PILING DATE: 1999-09-15 |
| PRIOR PILING DATE: 1999-09-15 |
| PRIOR PILING DATE: 1999-10-15 |
| PRIOR PILING DATE: 1999-11-29 |
| PRIOR PILING DATE: 1999-11-20 |
| PRIOR PILING DATE: 1999-11-20 |
| PRIOR PILING DATE: 1999-12-02 |
| PRIOR PILING DATE: 1999-12-02 |
| PRIOR PILING DATE: 1999-12-06 |
| PRIOR PILING DATE: 1999-12-07 
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83.3%; Score 230; DB
Best Local Similarity 100.0%; Pred. No. 6.1
Matches 230; Conservative 0; Mismatches
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APPLICANT: Genentech, Inc.; APPLICANT: Ashkenazi, Avi J.
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APPLICANT: SOY, MARGREE AND APPLICANT: SOY, MARGREE AND APPLICANT: SEWARTE, Timothy A. APPLICANT: Stewarte, Timothy A. APPLICANT: Stewarte, Timothy A. APPLICANT: Stewarte, Timothy A. APPLICANT: Tummas, Daniel D. Makey I. APPLICANT: Wood, Williams, P. Mickey I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE REPRENCE: 1046-104-106

TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION NUMBER: 05/09/665.350

PRIOR PELICANTON NUMBER: 05/09/00-18

PRIOR PELICANTON NUMBER: PCT/US99/2054

PRIOR PELICANTON NUMBER: PCT/US99/2054

PRIOR PELICANTON NUMBER: PCT/US99/2031

PRIOR PELING DATE: 1999-00-15

PRIOR APPLICATION NUMBER: PCT/US99/2031

PRIOR PELING DATE: 1999-10-05

PRIOR PE
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83.3%; Score 230; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 6.1e-217;
Matches 230; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapien
US-09-902-853-64
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APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Marcin L.

APPLICANT: Napier, Mary A.

APPLICANT: Tumas, Daniel

APPLICANT: Wapier, Mary A.

APPLICANT: Wapier, Mary A.

APPLICANT: Wapier, Mary A.

APPLICANT: Wapier, Mary A.

TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT

TITLE OF INVENTION: OF DISAASES CHARACTERIZED BY A33- RELATED ANTIGENS

TITLE OF INVENTION: OF DISAASES CHARACTERIZED BY A33- RELATED ANTIGENS

FILE REPERBRUCE: 102/09/254,465

FRICH REPLICATION NUMBER: US/09/254,465

PRIOR FILING DATE: 1999-03-05

PRIOR PRILNG DATE: 1999-11-20

PRIOR PAPLICATION NUMBER: US 60/066,364

PRIOR FILING DATE: 1998-11-21

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-17

PRIOR FILING DATE: 1998-03-17

PRIOR FILING DATE: 1998-03-17

PRIOR FILING DATE: 1998-03-17

PRIOR FILING DATE: 1998-03-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 312;
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Godowski, Paul J.
Grimaldi, Christopher J.
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; Publication No. US20020192659A1
; GENERAL INFORMATION:
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.4
Matches 230, Conservative
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APPLICANT: Ashkenai, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-499-9
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Gaps

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Length 312; Indels

Score 230; DB 10; L Pred. No. 6.1e-217;

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ONLEBDIVILEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLEN 156
                                                                                                                                                                                                                                         37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 6.1
Matches 230; Conservative 0; Mismatches
                         ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-64
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LENGTH: 312
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                                                                                                                                 Query Match
Best Local 8
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APPLICANT: Roy, Wargaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Pumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION WARRER: US/66,350
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PRING MARIET POLOSO-04-18
PRIOR PALICATION NUMBER: PCT/US99/2054
PRIOR PALICATION WARRER: PCT/US99/2054
PRIOR PALICATION WARRER: PCT/US99/2054
PRIOR PALICATION WARRER: PCT/US99/2054
PRIOR PALICATION WARRER: PCT/US99/2069
PRIOR PLICATION WARR
                                    Sequence 64, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Achkenazi, Avi
APPLICANT: Desneyers, Luc
APPLICANT: Desneyers, Luc
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Mather, Jennie P.
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119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
                                                                        157 PRLGSQSTINSSYTMINTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216
                                                                                                             179 PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/907, 841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
                                                                                                                                                                                     217 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 266
                                                                                                                                                                                                                     239 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR PRIOR APPLICATION NUMBER: PT/US99/20594
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
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Publication No. US20020198366A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-10-15
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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PRIOR APPLICATION NUMBER: 09/665,350
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Publication No. US20030003530A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, A.
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Best Local Similarity 100.
Matches 230; Conservative
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Gao, Wei-Qiang
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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97 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156
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83.3%; Score 230; DB 11; DB BBSt Local Similarity 100.0%; Pred. No. 6.1e-217;
Matches 230; Conservative 0; Mismatches 0;
              PRIOR PELICATION NUMBER: PCT/USO0/04414
PRIOR PELICATION NUMBER: PCT/USO0/0413,048
PRIOR PLING DATE: 1099-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
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PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
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2000-09-18
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-904-011-64
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December 9, 2003, 17:33:14; Search time 13.4634 Seconds (without alignments) 1971.458 Million cell updates/sec
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276
1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                       OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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Description

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Query Score Match Length DB

Result No. No matches found

SUMMARIES

Search completed: December 9, 2003, 17:38:32 Job time : 14.4634 secs

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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9, 2003, 17:26:43; Search time 9.61672 Seconds (without alignments) 1349.666 Million cell updates/sec
  - protein search, using sw model
                                         December
  protein
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US-09-852-797-76_COPY_23_298

276 1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276 score:

Scoring table: Sequence:

127863 segs, 47026705 residues Searched:

Gapop 60.0 , Gapext 60.0

30 ţ, Word size :

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult Query No. Score Match Length DB ID Description	P57087 homo sapie
ΙD	298 1 JAM2 HUMAN
图	-
Length	298
Query	240 87.0
sult No. Score Match Length DB ID	240
Result No.	1

: E

ALIGNMENTS

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TISSUE=Vascular endothelial cells;
MEDLINE=2011114; PubMed=10779521;
Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
Vascular endothelial junction associated molecule, a novel member the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells."

J. Biol. Chem. 275:19139-19145(2000).
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Junctional adhesion molecule 2 precursor (Vascular endothelial
junction-associated molecule) (VE-JAM).
                     298 AA
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=20507930; PubMed=10945976;
                   STANDARD;
                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                             Homo sapiens
                   JAM2 HUMAN
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                 P570<u>8</u>7;
JAM2_HUMAN
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REPUBLICE FROM N.A.

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REPUBLICATION OF TISSUE-Lung;

REPUBLICATION OF TISSUE TO THE TISSUE-Lung;

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Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjercke R.J., Vanderslice P., Morris A.P., Brock T.A., "A novel protein with homology to the junctional adhesion molecule: Characterization of leukocyte interactions."; J. Biol. Chem. 275:34750-34756(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-1- DATABASE: NAME-PROW; NOTE-PROW 2:1-3(2001);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
JUNCTIONAL ADHESION MOLECULE 2.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
POTENTIAL.
POTENTIAL.
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SWART; SW00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005887; C:integral to plasma membrane; NAS. GO; GO:0016337; P:cell-cell adhesion; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF255910; AAF81223.1; -. EMBL; AY016009; AAG49022.1; -. EMBL; BC017779; AAH17779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Ig-2.
InterPro; IPR003006; Ig_MHC.
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                                                                                                157 PRLGSOSTNSSYTWNTKTGTLOFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216
                                                                                                                                                                                                       GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
                                                                              Gaps
98 98 N-LINKED (GLCNAC. .) (POTENTIAL)
187 187 N-LINKED (GLCNAC. .) (POTENTIAL)
236 236 N-LINKED (GLCNAC. .) (POTENTIAL)
298 AA, 33207 MW, CA78E518E22DCAEE CRC64;
                                                                             ö
                                                    Query Match 87.0%; Score 240; DB 1; Length 298; Best Local Similarity 100.0%; Pred. No. 1.6e-232; Matches 240; Conservative 0; Mismatches 0; Indels
CARBOHYD
CARBOHYD
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SEQUENCE
FFFS
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Search completed: December 9, 2003, 17:36:26 Job time : 9.61672 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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December 9, 2003, 17:32:33 ; Search time 35.101 Seconds (without alignments) 2029.071 Million cell updates/sec
                                                                                                                    US-09-852-797-76_COPY_23_298
276
1 YHKAYGFSAPKDQOVVTAVX......SSKATTMSENDFKHTKSFII 276
OM protein - protein search, using sw model
                                                                                                                        Title:
Perfect score:
                                        Run on:
```

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

Sequence:

830525 segs, 258052604 residues Searched:

Word size : Sand 30

Đ, Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: sparchea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_lnvertebrate:*
6: sp_mamman:*
7: sp_mhc:*
7: sp_hage:*
9: sp_phage:*
10: sp_plant:*
10: sp_rodent:*
2: sp_virus:*
2: sp_virus:*
3: sp_vertebrate:*
3: sp_vert

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB Result

ID

Description

No matches found

Search completed: December 9, 2003, 17:38:06 Job time : 35.101 secs

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Location/Qualifiers
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Misc-difference 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9, 2003, 17:13:47; Search time 36.5436 Seconds (without alignments) 1198.803 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-emb1/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-emb1/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-emb1/AA1981.DAT:*
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| SIDSI/gcgdata/geneseq-emb1/AA2000.DAT:*
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276
1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters: * . . . 40
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1107863 seqs, 158726573 residues
                                                                                                                                      OM protein - protein search, using sw model
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		Description	Human secreted pro	Human dene 25 enco	Human dene 25 enco	Human genreted nro	Human secreted pro	Human dene 162 end	Secreted protein a	Human junctional a	Human polypeptide
SUMMARIES	£	7	AAW75220	AAE26983	AAE27121	ABR47926	ABU64994	ABR00172	AAW85457	AAU00512	ABP61801
	<u>a</u>	;	19	23	23	24	24	24	19	22	23
	Query Match Length DB 1	TI STORY	298	298	298	298	298	298	298	298	298
,	Query	110000	99.3	99.3	99.3	99.3	99.3	99.3	87.0	87.0	87.0
	0. 0.10	2 1	274	274	274	274	274	274	240	240	240
	Result		н	7	m	4	5	9	7	8	6

/label= unknown /label= unknown

Misc-difference 58

WO9840483-A2

97US-0068368. 97US-0040710. 97US-0040762. 97US-0048100.

19-DEC-1997; 14-MAR-1997; 14-MAR-1997; 30-MAY-1997;

98WO-US04858

12-MAR-1998; 17-SEP-1998

10	240	87.0	29		AA016452	Human	junctional a
11	230	83.3			AAY08060	Human	S.
15	230	83.3			AAY23324	a	lated antige
7 7	230	5.00			AAI 13354	Amino	acid sequenc
12	230	0 60			AAB23421		PRO245 prote
16	230	83.3			AAY70668		
17	230	83.3			AAU12339		
18	230	83.3	312	2 2	AAU00821		immune respo
20	230	0.00			AAB50904	Human	PRO245 proce
21	230	83.3			AAB53081		a
22	230	83.3			ABU69632		human secret
23	230	83.3			ABU71455		PRO polypept
24	230	83.3			ABU71901	Human	secreted/tra
25	230	83.3			ABU07738		A-33 related
26	230	83.3			ABU66737		PRO polypept
27	230	83.3			ABU67013		secreted/tra
28	230	83.3			ABU67355		
50	230	83.3			ABU59818		secreted and
30	230	83.3			ABU64509		secreted/tra
17	230	83.3			ABU54357		secreted/tra
32	222	80.4			AAM41947	Human	polypeptide
	215	6.77			AAB70500	Angiog	Angiogenesis prote
4) (183	66.			AAB27277	-	confluency r
η (P	166	60.1			AAM23693		EST encoded
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n c	ט ה	0.0			ABG22339		
? ?	TC	70.0				Novel	numan diagno
					ALIGNMENTS		
RESULT 1							
•	75220	andarc	standard; Protein;		298 AA.		
AC AAW	AAW75220;						
	29-JAN-1999	(first	cat entry)	2			
DE Hum	Human secreted protein encoded by	ted pr	otein e	popue	gene 25	clone HTEEB42.	
	Himan . goor	t pod a	. rototo.				
	all; bect	מרמה ל	Torein'	977	ion procein; gene cr		therapy;
	gnosis;	c188u6	; cance	ir;	diagnosis; tissue; cancer; tumour; neurodegenerative	ative disorder;	; leukaemia;
	eropmenc	al abr	ormalıt	й. Х	Setal deficiency; b	lood; allergy;	renal;
	une ByBr	em; as	L Duma;	, ympn	immune system; astrama; lymphocytic disease; brain; hepatic; lymphoma;	in; hepatic; i)	утрьота;
	Lammario	n; 180	naemic	Buoc.	t; Alzheimer's disea	ase, restenosia	s; AIDS;
	nicive a	Borde	ir; scni	zobu	cognitive disorder; schizophrenia; prostate; obesity; osteoci	-	ast; thymus;
	eoporosı.	B; art	nritis;	rea	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid;		digestion;
	ocrine;	metabo	118m; 1	egur	tion; malabsorption		neoplasm.
	Homo caping						
	o sapien						
1		•	7 4 6 7	,			

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Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer; grave's disease; diabetes mellitus; hematopoietic disorder; stroke; respiratory disorder; asthma; allergy; gastrointestinal disorder; inflammatory bowel disease; heurodegenerative disorder; hepatitis; parknon's disease; Alzhaimer's disease; cardiovascular disorder; atherosclerosis; myocarditis; renal disorder; fungicide; virucide; hyperproliferative disorder; acute glomerulonephritis; tonsilitis; respiratory disorder; hinitis; sinusitis; neurological disease; endometriosis; vasotropic; vulnerary; cytostatic; nootropic; cardiant; anti-HIV; tranquilliser; gout; antiparasitic.
                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2001; 2001US-0852659
                                                                                                                                                                                                                                                                                                                          Misc-difference 58
                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                               US2002077287-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-1998;
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2002
                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RUBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZENG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIYY/
    This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 28 novel genes and their fragments (nucleic acid sequences: AAV3426-V3435; amino acid sequences AAW75196-W75235) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polymucleotides. Specific uses are described for each of the 28 polymucleotides. Specific uses are described for each of the 28 polymucleotides. Dased on which tissues they are most highly expressed in
                                                                                                                                                                                                      Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
                                                                                                           Fischer CL, Gentz RL, Greene JM, Kyaw H;
, Moore PA, Rosen CA, Ruben SM, Soppet DR;
                                                                                                                                                                                                                                                                Claim 1; Page 168-169; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (see AAV34286 for described uses)
97US-0048189.
97US-0048357.
97US-0050934.
97US-0048970.
97US-005776S.
                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                         Zeng Z;
                                                                                                                                                                  WPI; 1998-520811/44.
                                                                                                                                      Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 AA;
                                                                                                                                                                               N-PSDB; AAV34310.
                                                                                                                         Li Y,
 30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
                                         06-JUN-1997;
05-SEP-1997;
                                                                                                             Ferrie AM,
                                                                                                                   , H,
YF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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23..298 /note= "Human mature secreted protein"

1..22 /label= Signal_peptide Location/Qualifiers

/label= Unknown /note= "Encoded by TSC"

98US-0152060.

RUBEN S M. ROSEN C A.

FISCHER C L.

ZENG Z. KYAW H.

(KYAW/) LIHH/)

LI H. SOPPET D R.

GENTZ R L.

(SOPP/) (GENT/)

(WEIX/)

/label= Unknown /note= "Encoded by GWG"

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                                                                                                                                 FRNRAEMIDFNIRIRRNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 142
                                                                                                                                                                                                                       TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
                                                                                                             FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGONLEEDTVTLEVLVAPAVPSCEVP 120
                                                                                                                                                                 SSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFN 180
                                                                                                                                                                                   1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD 60
                                                                                    82
                                                                     23 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                              Gaps
                              ô
99.3%; Score 274; DB 19; Length 298; 100.0%; Pred. No. 1.2e-260;
                           0; Indels
                                                                                                                                                                                                                                                                                                RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
        100.0%; Pred. .v..
             Local Similarity 100.
nes 276; Conservative
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 Query Match
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Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.

(first entry)

13-DEC-2002

XEXEXEX

AAE26983;

\$

AAE26983 standard; Protein; 298

AAE26983 RESULT

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AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted protein genes, and AAE26959-AAE2699 represent the proteins they encode. AAE27000-AAE27025 represent human secreted protein fragments or their variants. The secreted proteins and genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed and include developing products for the diagnosis or treatment of immunodeficiencies, e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe or y. X-linked agammaglobulinaemia, multiple sclerosis, autoimmune erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
                                                                                                                                                                                                                                                                                                                   Novel human secreted polypeptides and polynucleotides for diagnosing, preventing, treating immune, hyperproliferative, cardiovascular, neurological, reproductive disorders and identifying modulators of
Li Y, Zeng Z, Kyaw H, Fischer CL, Li F
Wei Y, Moore PA, Young PE, Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 186; 209pp; English.
Rosen CA,
Gentz RL,
                                                                                                                                                                                   WPI; 2002-598780/64.
                                                                                                                                                                                                                                   N-PSDB; AAD44660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic use
                                                    В,
                                                    Soppet DR,
Ferrie AM;
    Ruben SM,
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TSC.

/note= "Encoded by

11-MAY-2001; 2001US-0853161. 02-FEB-2001; 2001US-265583P.

LI Y.
ZENG Z.
KYAW H.
FISCHER C L.

(KYAW/) (FISC/)

ZENG/

RUBEN S M. ROSEN C A.

(RUBE/) (ROSE/)

SOPPET D R. GENTZ R L. WEI Y. MOORE P A. YOUNG P E.

(SOPP/) (GENT/) MOOR/)

WEIY/)

(LIHH/)

/label= Unknown

Misc-difference

US2002076756-A1 20-JUN-2002

/note= "Encoded by GWG'

/label= Unknown

Misc-difference 42

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including septic shock, sepsis, reperfusion injury, inflammatory bowel disease, chematopoietic disorders, respiratory disease, chon's disease, haematopoietic disorders, respiratory asthma and allergy, gastrointestinal disorders e.g., inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and breast), central nervous system (CNS) disorders e.g., lacker in the properties of the present sequence of the properties of the invention.

Inver disorders, endocrine disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism, infectious diseases and reproductive system disorders e.g. endometriosis. The present sequence represents a human secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FKNRAEMIDFNIRIKANVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
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100.0%; Pred. No. 1.2e-260;
ive 0; Mismatches 0;
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Best Local Similarity 100."
Matches 276; Conservative
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Human; secreted protein; autoimmune disease; hyperproliferative disorder; rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis; cerebral ischaemia; cardiovascular disorder; nervous system disorder; cardiac arrest; Alzheimer's disease; ocular disorder; wound healing; infection; corneal infection; skin aging; food additive; preservative; tissue regeneration; immunosuppressive; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
                                                                                                                                                                                                                                                                                  (first entry)
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AAE27121 standard; Protein; 298 AA

AAE27121;

/label= Signal_peptide 23..298 /note= "Mature human secreted protein"

Protein Peptide

Location/Qualifiers

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AAD44954-AAD44984 represent cDNAs corresponding to 29 human secreted protein genes, and AAE27137 represent the proteins they encode. AAE27139-AAE27137 represent the proteins they encode. AAE27164 represent human secreted proteins tragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Secreted protein sequences of the invention are useful for the diagnosis or treatment of disorders such as autoimmune diseases (e.g. the matoid arthritis), hyperproliferative disorders (e.g. neoplasms of the breast or liver), cerebrovascular disorders (e.g. cerebral isofaemia, angiogenesis), cardiovascular disorders (e.g. cerebral isofaemia, polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs to regenerate tissues and in chemocravis. They concern transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemocravis. They can also be used as food additives or preservative to increase or decrease storage capabilities, and orther mitting protein, carbohydrate, vitamins, minerals, cofactors humans and orther mitting and encourants and orther angelia content, and any orthers. They can also be used as food and orther mitting and encourants and orther mitting and encourants and orther angelia content, and any orthers. They can also be abed as food and orther mitting and encourants and are accounted and orther angelia content, and any orthers. They can also be abed as food and orther and any orthers and any orthers and any orthers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 186-187; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein of the invention.
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Matches 276; Conservative
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nucleic acid molecules encoding 28 human secreted proteins, useful diagnosing, preventing, treating or ameliorating medical conditions as food additives or preservatives

Li Y, Zeng Z, Kyaw H, Fischer CL, Li I Wei Y, Moore PA, Young PE, Greene JM;

A CA,

Rosen CP Gentz F

Soppet DR, Ferrie AM; Ruben SM,

GREENE J M. FERRIE A M.

(YOUN/) (GREE/)

(FERR/)

WPI; 2002-574454/61.

N-PSDB; AAD44878

for

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The present invention relates to novel human secreted proteins

(ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The

proteins and their coding sequences are useful for the preparation of a

diagnostic or pharmaceutical composition for diagnosting or treating a

cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,

cardiovascular disorders, muscular disorders, reproductive disorders,

immune system disorders, pulmonary disorders, reproductive disorders,

cardiovascular disorders, pulmonary disorders, reproductive disorders,

cy anstrointestinal disorders, pulmonary disorders, renal disorders,

proliferative disorders and/or cancerous disease and conditions, for

continual disorders and/or cancerous disease and conditions, for

infection, for treating thrombosis and arteriosclerosis, for treating or

continual damage which occurs in neuronal disorders or

neurodegenerative conditions such as Alzheimer's disease and Parkinson's

disease, to enhance bone and periodontal regeneration and aid in tissue

transplants or bone grafts, to prevent skin aging or hair loss, to

stimulate growth and differentiation of haematopoietic cells and bone

marrow cells when used in combination with other cytokines, to maintain
                                                                      180
                                                                                                                                             240
                                  142
                                                                                                         202
                                                                                                                                                                Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
                   TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ
FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                   SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia -
                                                                                                                                                                                                                                     RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein, SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; rheumatoid arthritis; diabetes mellitus; heematopoietic disorder; inflammatory condition; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; lschaemic brain injury; neurodegenerative disorder; Parkinson's disease; blood-related disorder; rhromboals; atheroselerosis; sincertated disorder; acute glomerulonephritis; Addison's disease; hyperproliferative disorder; acute glomerulonephritis; Addison's disease; endocrine disorder; liver disease; reproductive system disorder; endomerriosis; infectious disease; reproductive system disorder; wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
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organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism.
                                                                                                                                                                                                                                                                                                              143 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFN
                                                                                                                                                                                                                                                                                                                                                                                                                       181 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ
                                                                                                                                                                                                                                                                23 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                              PKNRAEMIDFNI RIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
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                                                                                                                                                                                                    Gaps
                                                                    Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                    Length 298;
                                                                                                                                                                 Score 274; DB 24; Length 2
Pred. No. 1.2e-260;
); Mismatches 0; Indels
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100.0%; Prer
0; N
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97US-040762P.
97US-048100P.
97US-048189P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                              Best Local Similarity 100.
Matches 276; Conservative
                                                                                                                                     298 AA;
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30-MAY-1997;
30-MAY-1997;
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14-MAR-1997;
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                                                                                                                                   Sequence
                                                                                                                                                                 Query Match
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The invention relates to an isolated polypeptide comprising an amino acid sequence at least 95% identical to sequence of 28 human secreted form, proteins, their fragment, polypeptide domain, epitope, secreted form, cariant, allelic variant, polypeptide domain, epitope, secreted form, cariant, allelic variant, polypeptide domain, epitope, secreted form, cariant, allelic variant, polypeptide domain, extended in ATCC 97921 and 97822. Also included are the encoding cariant and proteins and nucleic acids are useful for diagnosing, preventing, creating pregnosing or ameliorating a medical condition e.g. treating prognosing or ameliorating amedical condition e.g. immunodeficiancies (e.g. X-linked agammaglobulinaemia, B cell immunodeficiancies) severe combined immunodeficiancies, multiple immunodeficiancies, severe combined immunodeficiancies, dermatitis, dermaticies, autoimmune thyroiditis, autoimmune hamolytic anaemia, conditions (e.g. systemic crythmatosyr conditions (e.g. septic shock, condessions), reperfusion injury, inflammatory conditions (e.g. septic shock, seppis, reperfusion injury, inflammatory conditions (e.g. septic shock, seppis, reperfusion injury, inflammatory conditions (e.g. septic shock, conditions), respiratory disorders (e.g. gasthma and allergy), gastrointestinal crythmatosyr conditions (e.g. septic shock, traumatic brain injury), neurodegenerative disorders (e.g. parkinson's disease and Alzheimer's disease, AlbS-related disorders (e.g. parkinson's disease and Alzheimer's disease, and cardoul ninyry and/or stroke, traumatic brain injury), neurodegenerative gancreaticis, arcidovascular disease, and cardoul cathersoclerosis, myocarditis, cardiovascular disease, and cardoul for stroke, traumatic pancreaticis, sarcoidosis, cardiovascular disease, and cardour cathersoclerosis, myocarditis, alloquic transplant rejection), hyperproliferative disorders (e.g. adue domentia, and prion disorders (e.g. adue domentia, and prion disorders (e.g. adue domentia, and pancreatic disorders (e.g. adue domentia, and p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human secreted polypeptides and polynucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                          Li Y, Zeng Z, Kyaw H, Fischer CL, Li N
Wei Y, Moore PA, Young PB, Greene JM;
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97US-050934P.
97US-048970P.
97US-057765P.
97US-068368P.
98WO-US04858.
98WO-US04858.
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Gentz RL,
                                                                                                                                                                                  ZENG Z.
KYAW H.
FISCHER C L.
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SOPPET D R.
GENTZ R L.
WEI Y.
MOORE P A.
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FERRIE A M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic use
                                                                                                                                    ROSEN
                                                                     02-FEB-2001;
                                                                                    12-MAR-1998;
                                                                                                   11-SEP-1998;
                                                   19-DEC-1997
                                   05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrie AM;
                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM,
                                                                                                                                  (RUBE/)
(ROSE/)
(LIYY/)
(ZENG/)
(KYAW/)
(FISC/)
(LIHH/)
                                                                                                                                                                                                                                                                                                     (MOOR/)
(YOUN/)
(GREE/)
                                                                                                                                                                                                                                                                       (GENT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; biliary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunosuppressive; vulnerary; chromosome 21q21.2.
capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                        TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ
                                                                                                                                                                                                    YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                             FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGONLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                               FKGNRAEMIDENIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP
                                                                                                                                                                                                                                                                                                        121 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN
                                                                                                                                                                                                                                                                                                                          143 SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSGSTNSSYTMYKTGTLQFN
                                                                                                                                                                                                                                                                                                                                                                      TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ
                                                                                                                                                                                1 YHKAYGFSAPKDQQVVTAVXYQEAILACKTPKKTVXSRLEWKKLGRSVSFVYYQQTLQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers -
                                                                                                                                                   Gaps
                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene 162 encoded secreted protein HTEEB42, SEQ ID NO:461.
                                                                                                                    Length 298;
                                                                                                                                                 Indels
                                                                                                               99.3%; Score 274; DB 24; L
100.0%; Pred. No. 1.2e-260;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    276
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Page 1046-1047; 1216pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR00172 standard; Protein; 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-277340P.
19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-2002; 2002WO-US08276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                 Conservative
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                                                                                                                Query Match
Best Local Similarity
                                                                                     298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABZ71351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-2003
                                                                                                                                                Matches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA,
                                                                                                                                                                                                                                             19
                                                                                      Sequence
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Direction genes, and ABP00011-ABP00299 represent the proteins they encode.

Maz71479-ABZ77478 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, and recombinant the use of the secreted proteins in drug screening, and recombinant to vectors and host cells comprising a mucleic acid of the invention. The secreted proteins in mucleic acid of the invention. The secreted proteins, and included secreted proteins and host cells comprising a mucleic acid of the invention. The secreted proteins, and include disorders of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, cosophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the treatment of immune disorders, and to promote wound healing. Nucleic acids by Preproliferative disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome cost the invention may be used for chromosome disorders, as hybridisation probes, and as molecular weight anxiets. The present sequence represents a human secreted protein of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 TVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDIANISGIIAAVVVVALVISVCGLGVCYAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suppressing activity; haematopoiesis regulating activity;
tissue growth activity; activin; inhibin activity; chemotactaxis;
chemokinetic activity; haemostasis; thrombolytic activity; receptor;
ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; nutritional activity; immune stimulating; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.3%; Score 274; DB 24; L
Best Local Similarity 100.0%; Pred. No. 1.2e-260;
Matches 276; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein encoded by clone ct864_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW85457 standard; Protein; 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ligand; anti-inflammatory; cadhetumour inhibition; gene therapy
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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The present sequence represents a secreted protein. The polynucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing or amaliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating activity, tissue succines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotratic/chemokinetc activity, activin/inhibin activity, activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion auppressor activity, anti-inflammatory activity, cadherin/tumour juvasion auppressor activity, and tumour inhibition activity (no data is given in the specification to support these activities). The polynucleotide is also stated to be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Junctional adhesion protein; JAM2; cellular localisation; cellular expression; immunoprecipitation; stroke; phosphorylation; glycosylation; paracellular migration; inflammatory disease; arthritis; asthma; rheumatoid arthritis; inflammatory bowel disease;
                                                                                                                                                                                    New polynucleotides encoding secreted human proteins - derived fro
human foetal brain, adult brain, foetal kidney, placenta or adult
pineal gland cDNA libraries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 298;
                                                                                              Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                            McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 240; DB 19;
Pred. No. 3e-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human junctional adhesion protein (JAM2).
                                                                                          Lavallie ER,
Treacy M;
                                                                                                                                                                                                                                                Claim 17; Page 73-74; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.0%; Scc.
100.0%; Pre
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                98US-0044466.
97US-0822167.
                                                            (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240; Conservative
                                                                                          J, Jacobe 1
Spaulding 1
                                                                                                                                     WPI; 1998-609890/51.
N-PSDB; AAV82780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crohn's disease.
                19-MAR-1998;
21-MAR-1997;
                                                                                          Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                         Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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The polynucleotide encoding the polypeptide is useful for recombinant production of JAM-2 protein, which in turn is useful for the production of antibodies may be used for probing cellular localisation and/or expression of JAM2 in tissues under normal and disease states, for immunopracipitating JAM2 protein from cells and/or stroke tissues to determine whether it is modified by glycosylation and phosphorylation, and for determining JAM2 function. The antibodies inhibit interaction of JAM2 with inflammatory cells or influences their paracellular mignation, and is therefore useful for alleviating inflammatory diseases such as arthritis, asthma, rheumatoid arthritis, inflammatory bowel disease and Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids encoding human junctional adhesion protein useful for producing antibodies that are suitable for therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a human junctional adhesion molecule 2 (JAM2)
                /note= "Possible signal peptide #1"
                                             'note= "Possible signal peptide #2"
                                                                                                             "Possible mature JAM2 #2"
                                                                                                                       237..254
/note= "Transmembrane domain"
                                                                              mature
                                                                                                                                                                                                                                                                                                                                     Cunningham S, Trindad Arrate Barros M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 46-47; 51pp; English
                                                                             "Possible
                                                                                                                                                                                                                                                                                                       (TEXA-) TEXAS BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                                                       99US-0150459.
                                                                                                                                                                                                                                         23-AUG-2000; 2000WO-US23158
                                                              21..298
                                                                                              29..298
                                                                                                              /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 AA;
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS00512
                                                                                                                                                                           WO200114404-A1.
                                                                                                                                                                                                                                                                       24-AUG-1999;
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                              Peptide
                                                              Protein
                                                                                              Protein
                                                                                                                              Domain
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                    ONLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLEN 156
                                                                                                                   96
                                                    37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
                                                                                                                                                    PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                                                                                   GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII
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        Score 240; DB 22; Length 298;
Pred. No. 3e-227;
                                0; Indels
87.0%; Scor.
100.0%; Pred. No. sc.
'... 0; Mismatches
                               Matches 240; Conservative
                  Local Similarity
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          Query Match
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ABP61801 standard; Protein; 298 AA.
                                         ABP61801
RESULT 9
ABP61801
ID ABP(
XX
AC ABP(
XX
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Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antilnflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulcer; funglcide; antidiabetic; antiasthmatic; antiallergic; immunostimulant; antiparastici; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.
                  Human polypeptide SEQ ID NO 155.
                                                                                                                                                                                          22-DEC-2000; 2000US-0745763.
                                                                                                                                                                                                             98US-0040963.
                                                                                                                                                                                                                                                           L A.
04-OCT-2002 (first entry)
                                                                                                                                                                                                                                                          COLLINS-RACIE
                                                                                                                                                                                                                                                                                     TREACY M. SPAULDING V.
                                                                                                                                                                                                                                                                  EVANS C.
MERBERG D.
                                                                                                                                                                                                                                        MCCOY J M.
LAVALLIE E
                                                                                                                                                                                                                               JACOBS K.
                                                                                                                                                      US2002065394-A1
                                                                                                                                      Homo Bapiens.
                                                                                                                                                                                                            18-MAR-1998;
                                                                                                                                                                        30-MAY-2002.
                                                                                                                                                                                                                                                                                    (TREA/)
(SPAU/)
                                                                                                                                                                                                                                                                  (EVAN/)
                                                                                                                                                                                                                              (JACO/)
                                                                                                                                                                                                                                                                             (MERB/)
                                                                                                                                                                                                                                                 (LAVA/)
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Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis Collins-Racie LA, LaVallie ER, Spaulding V; Treacy M, WPI; 2002-582343/62. N-PSDB; ABQ92017 Jacobs K, Merberg D,

Evans C;

McCoy

Claim 54; Page 116-117; 284pp; English.

The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or ameliorating a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activity no rinhibin-related activities. (I) can be used to manipulate stem cells in culture to give rise to neurospithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. (I) induces the proliferation of neural cells and cells damaged by illness, autoimmune disease, and rearment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Muntington's disease, amyotrophic central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Muntington's disease, amyotrophic activity, regulation of haematopolesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia cor lymphoid cell disorders, platelet disorders such as thrombocytopaenia cor lymphoid cell disorders, platelet disorders such as thrombocytopaenia cor treating osteoporosis, osteoarthrisis, bone degeneration or regeneration and treatment of lung or liver fibrosis, reperfusion injury cor regeneration and treatment of lung or liver fibrosis, reperfusion injury cor vergeneration and disorders or liver fibrosis, reperfusion injury con various immune disorders and disorders including autoimmune disorders e.g. multiple sclerosis, rheumatoid arthriss.

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Gaps

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treatment

(huJAM)

178

216

276 298

118 156

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inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inflammatory cell infiltration; immune response; T cell proliferation; anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOG
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       immune deficiency or an inflammatory disorder, cancer, wound healing or a cardiovascular disease
                                                                                                             The invention comprises the DNA and protein sequences of the extracellular region of human junctional adhesion molecules (huJAM). extracellular huJAM DNA and protein sequences are useful in the tree of: immune system disorders (e.g. immune deficiency); autoimmune disorders; inflammatory disorders; cancer; wound healing; or a cardiovascular disease. The present amino acid sequence represents full-length membrane-bound huJAM2 protein.
                                                                                                                                                                                                                                                                                                                                                   Query Match 87.0%; Score 240; DB 24; Length 298; Best Local Similarity 100.0%; Pred. No. 3e-227; Matches 240; Conservative 0; Mismatches 0; Indels
                                                                          Disclosure; Fig 1; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY08060 standard; Protein; 312
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97US-0053263.
97US-0063550.
97US-0066364.
97US-0066364.
97US-0066770.
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24-NOV-1997;
04-JUN-1998;
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28-OCT-1997;
12-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene therapy; extracellular region; junctional adhesion molecules; huJAM; immune system disorder; immune deficiency; autoimmune disorder; inflammatory disorder; cancer; wound healing; cardiovascular disease; full-length membrane-bound huJAM protein.
diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as athma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention.
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                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                87.0%; Score 240; DB 23;
100.0%; Pred. No. 3e-227;
iive 0; Mismatches 0;
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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05-FEB-2002; 2002US-354345P
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                                                                                                                                                                                                                                240; Conservative
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                                                                                                                                     298 AA;
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AAY23324 standard; Protein; 312 AA

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This invention describes a novel composition containing (apart from a carrier or excipient), a novel PRO245 polypeptide [1], its agonist or antagonist, or their fragments, for modulating: (i) infiltration of antagonist, or their fragments, for modulating: (i) infiltration of the effects of inflammatory cells into cissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects [1]-[iii]. The products of the invention have anti-inflammatory of the effects anti-autoimmune and anti-diabetic activity. (I), and its (ant) agonists and their fragments, are used to treat immune-related diseases.

Conticularly T cell-mediated diseases treated include systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies (dermatomyositis, juvenile chronic arthritis, spondyloarthropathies (dermatomyositis, juvenile chronic arthritis, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemolytic anemia (immune pancytopenia, paroxysmal nocturnal chronic hemolytic anemia (immune pancytopenia, thyroiditis, artophic control of thyroiditis, juvenile lymphocytic thyroiditis, artophic control of thyroiditis, juvenile lymphocytic thyroiditis, artophic control of thyroiditis, juvenile lymphocytic thyroiditis, artophic dispathic demyelinating polyneuropathy, Guillan-Bare syndrome, chronic active hepatinas polyneuropathy, infectious hepatitis, indiametory demyelinating polyneuropathy, infectious hepatitis, demonic active hepatitis, pand solerosing cholangitis, inflammatory bowel disease including chronic active hepatitis, pand solerosing cholangitis, inflammatory bowel disease including chronic active hepatitis, pand solerosing cholangitis, inflammatory bowel disease including curicaria eosinophilic proteinne mediated for dispancia enteropathy, and transplantation associated diseases confragence and solerosing and dispance and addivent 
                                                                                                                                                                                                                                                                                                                                                    Composition containing novel polypeptide PRO245, its agonist or
                                                                                                   Wood WI;
                                                                                                   Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 2; 177pp; English
                                                                                                   Gurney AL,
(GETH ) GENENTECH INC
                                                                                              Goddard A,
                                                                                                                                                                                            WPI; 1999-229499/19.
N-PSDB; AAX37664.
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                                                                                                                                                                                                                                                                           0; Gaps
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RESULT 12 AAY23324

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The specification describes A33 related antigens PRO301, PRO362 and PRO245. The methods and compositions of the invention are useful for the PRO245. The methods and compositions of the invention are useful for the C reatment and diagnosis of inflammatory disease and tumours in mammals. Such inflammatory diseases include of inflammatory bowel disease, c Such inflammatory diseases include of inflammatory bowel disease, c Such inflammatory wypathies, systemic scherosis, solvenile chronic arthritis, spondyloarthropathies, systemic scherosis, polymyositis, cidiopathic inflammatory myopathies, dermatomyositis, polymyositis, comman, immune pancytopenia, paroxysmal nocturnal hemoglobinuria, anemia, immune pancytopenia, idiopathic thrombocytopenic purpura, immune pancytopenia, idiopathic thrombocytopenic purpura, immune mediated thrombocytopenia, thyroiditis, Grave's disease, immune-mediated disease, c Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis, dabetes mealitus, immune-mediated meal disease, infectious hepatitis cof the central and peripheral nervous systems such as multiple sclerosis, cidiopathic polymeuropathy, hepatobiliary diseases, infectious hepatitis cof hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cof cholangitis, inflammatory and fibrotic lung diseases, gluten-sensitive enteropathy, Whipple's diseases altomatous hepathic pulmonary fibrosis and hypersensitivity pneumonitis cransplantation associated diseases disease. The present sequence cor ransplantation associated diseases disease. The present sequence
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                                                                                                                                                A33 related antigen; PRO301; PRO362; PRO245; inflammatory disease;
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100.0%; Pred. No. 2.1e-217;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigens PRO301, PRO362 and PRO245 related to A33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 11; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                98WO-US19437.
97US-0066364.
98US-0078936.
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                                                                                                           A33 related antigen PRO245.
                                                                       02-SEP-1999 (first entry)
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Best Local Similarity 100.'
Matches 230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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                                                                                                                                                                                                     Homo sapiens.
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21-NOV-1997;
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                                    AAY23324;
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216
                    238
PRIGSOSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
           PRLGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS
                                                                                                                                                                               Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvilus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                    GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 266
                                               Amino acid sequence of protein PRO245.
                                                                                                       AAY13354 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                 97US-0059113.
97US-0059115.
97US-0059117.
97US-0059119.
97US-0059121.
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970S-0059184.
970S-0059263.
970S-0059266.
970S-0062125.
970S-0062285.
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97US-0062814.
97US-0062816.
97US-0063045.
97US-0063120.
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970S-0063435.
970S-0063704.
970S-0063732.
970S-0063738.
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97US-0064215.
97US-0063735.
97US-0063870.
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                                                                                                                                            (first entry)
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24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
27-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
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17-OCT-1997;
17-OCT-1997;
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18-SEP-1997;
18-SEP-1997;
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29-OCT-1997;
29-OCT-1997;
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17-SEP-1997;
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                                                                                                                          AAY13354;
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                  179
                                    217
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AAY13344-403 represent secreted and transmembrane human proteins.

The CDNA sequences are obtained from CDNA libraries, prepared from

CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

CT he encoded polypeptides have specific uses based on their homology to

Known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

CC sasociated with the preservation and maintenance of gastrointestinal

CC ucatated with the preservation and maintenance of gastrointestinal

CC ucatation and congenital microvillus strophy), skin diseases associated

With abnormal keratinocyte differentiation (e.g. psoriasis, epithelial

CC ucatation and congenital microvillus arrophy), skin diseases associated

With abnormal keratinocyte differentiation (e.g. psoriasis, epithelial

CC ptent effects on cell growth and development, diseases related to

CC profit fibromodulin, e.g. for reducing derand scarring. PRO266 can be used as

CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as

CC for fibromodulin, e.g. for reducing derand secarring. PRO264 can be used

CC USHER Syndrome or Atrophia areata; PRO333 may be used in the treatment

CC USHER Syndrome or Atrophia areata; PRO353 may be used as an

CC anti-thrombotic agent; PRO387 polypeptides and portions may have

CC therapeutic applications in wound healing and tissue repair; PRO317 can

CC be used for treating problems of the kidney, uterus, endometrium, blood

CC vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and polypeptides used in, e.g. treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 266
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                                                                                                                                                                                                                                                                           Yuan
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                                                                                                                                                                                                                                                                             Wood
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                97US-0064248.
97US-0065186.
97US-0065186.
97US-0065693.
97US-0066364.
97US-0066364.
97US-0066772.
97US-0066772.
 97US-0064103
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                                                                                                                                                                                                                                                                                                                                                                               gastrointestinal ulceration
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Best Local Similarity 100.0
Matches 230; Conservative
                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
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                              07-NOV-1997;
12-NOV-1997;
17-NOV-1997;
18-NOV-1997;
21-NOV-1997;
24-NOV-1997;
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RESULT 14 AAB33421

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Ademostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipociatic; antiallergic; antianaemic; hepatotropic; virucide; antipociatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloathropathy; systemic solerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vascullis; autoimmune haemolyptic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Mhipple's disease; inflammatory bowel disease; pluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immune-mediated skin disease; allergic disease; immunelogical disease; transplantation associated disease;
                                                                                                 cardiant;
                                                                                                          dermatological; antiarthritic; antirheumatic; immunosuppressive;
                                                                                              Human; immune related disease; diagnosis; antiinflammatory;
                                                                                                                                                                                                                                                           graft rejection; graft-versus-host-disease
                                                                       Human PRO245 protein UNQ219 SEQ ID NO:36.
 AAB33421 standard; Protein; 312 AA
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99US-0123618.
99US-0123957.
99US-0125775.
99US-0128849.
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99US-0131445.
99US-0132371.
99US-0134287.
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2000WO-US00376
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                                                 (first entry)
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20-APR-1999;
28-APR-1999;
04-MAY-1999;
14-MAX-1999;
23-JUN-1999;
26-JUL-1999;
28-JUL-1999;
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20-DEC-1999;
30-DEC-1999;
05-JAN-2000;
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29-OCT-1999;
29-NOV-1999;
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15-SEP-1999;
15-SEP-1999;
                                               29-JAN-2001
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02-DEC-1999;
02-DEC-1999;
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                        AAB33421;
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(GETH) GENENTECH INC

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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-PRO antibodies, agonists and antagonists are useful for treating and disgnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central and peripheral nervous systems, hepatobiliary diseases inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune-mediated skin diseases allergic diseases, immunological diseases of the lung, and transphantation associated diseases including graft rejection and graft-versus-host-disease. AACS8519 to AACS8518 represent PKP primers and hybridisation probes used in the isolation of human PRO sequences. AACS8579 to AACS8642 and AACS8642 and AAB33477 represent human PRO polymuclectide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIRNVTRSDAGKYRCEVSAPSEQG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                 Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
    Henzel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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KP, Goddard A, Gurney AL, Hebert C, He
Pan J, Pennica D, Shelton DL, Smith V;
, Watanabe CK, Wood WI, Yan M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN
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                                                                                                                                                                                                                                      Claim 33; Fig 16; 309pp; English.
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ses 230; Conservative
    Baker KP,
               Kabakoff RC, Lu Y, Pastewart TA, Tumas D,
                                                                                       2000-572271/53.
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                                                                                                           N-PSDB; AAC58586
    Ashkenazi AJ,
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endochelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endochelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors ansociated with decreased PRO expression. AAA77510 to AAA77721 and AAB2438 to AAB2438 to ABA2435 represent nucleotide and protein sequences used in the example of the argument of the encoders.
                                                                                                                                                                                                                                                                                                                                                                                                      Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                   Gerber H, Hillan KJ, Goddi
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.3%; Score 230; DB 21; Length 312; 100.0%; Pred. No. 2.1e-217; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP, Ferrara N,
Gurney AL, Klein RD,
Williams PM, Wood WI;
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                                                                                    98WO-US25108.
98US-0112554.
99US-0115554.
99WO-US05028.
99US-0131957.
99WO-US1252.
99US-01441037.
99WO-US1252.
99US-0144758.
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99WO-US23089
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Best Local Similarity
Matches 230; Conserva
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WO200032221-A2
                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi AJ,
                                                                                                                12 - JAN - 1999)
08 - MAR - 1999)
18 - APR - 1999)
14 - MAY - 1999)
02 - JUN - 1999)
23 - JUN - 1999)
20 - JUL - 1999)
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01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
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Watanabe CK,
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15-SEP-1999;
05-OCT-1999;
                                                          30-NOV-1999;
                             08-JUN-2000
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Gaps

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ONLEEDTVILEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWFKDGIRLLEN 156 PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216

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157 179

37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDPNIRIKNVTRSDAGKYRCEVSAPSEQG 96

Conservative

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239 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSEN 288
217 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN
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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Word size :

Searched:

Database :

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JOHNSANL INFORMATION:
JAPPLICANT: Ashkenazi, Avi J.
JAPPLICANT: Ashkenazi, Avi J.
JAPPLICANT: Cenestech, Inc.
JAPPLICANT: Cond. Sherman
APPLICANT: Goddard, Audrey
JAPPLICANT: Goddard, Austin L.
JAPPLICANT: Gurney, Austin L.
JAPPLICANT: Wood, William I.
JAPPLICANT: Wood, William I.
JAPPLICANT: TILE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
JITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
JAPPLICANT: MORBER: US/09/254,465A
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR APPLICATION NUMBER: US 60/066,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-152-060-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 FKNRAEMIDENIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 RKGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 298
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-06-30
EARLIER PILING DATE: 1997-09-06
EARLIER APPLICATION NUMBER: 60/05,765
EARLIER APPLICATION NUMBER: 60/068,970
EARLIER PILING DATE: 1997-09-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 76
EARLIER PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 76
LENGTH: 298
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; Patent No. 6410708
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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Sequence 9, Appli
                                                                                                                                                                                   December 9, 2003, 17:22:07; Search time 13.9443 Seconds (without alignments) 837.463 Million cell updates/sec
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276
1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
// cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
// cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
// cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
// cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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// cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P1.03

CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT PILING DATE: 1998-09-11

EARLIER FILING DATE: 1998-03-12

EARLIER FILING DATE: 1998-03-12

EARLIER FILING DATE: 1997-03-14

EARLIER APPLICATION NUMBER: 60/040,710

EARLIER APPLICATION NUMBER: 60/040,710

EARLIER PILING DATE: 1997-03-14

EARLIER PILING DATE: 1997-03-14

EARLIER PILING DATE: 1997-05-30

EARLIER PILING DATE: 1997-05-30

EARLIER PILING DATE: 1997-05-30
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US-09-254-465A-9
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                                                                                                                                    OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:

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APPLICATION TO BE Human Secreted Proteins TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: PEOU3P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR PELLING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
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PRIOR PLING DATE: 1997-03-14
PRIOR PLING DATE: 1997-03-16
PRIOR PLING DATE: 1997-05-30
PRIOR PRIOR PRESENTING DATE: 1997-05-30
PRIOR PRIOR DATE: 1997-05-30
PRIOR PRIOR PRESENTE: 1997-05-30
PRIOR PRIOR PRESENTE DATE: 1997-05-30
US-09-906-742-64

US-09-906-818-64

US-09-907-818-64

US-09-907-942-64

US-09-907-859-64

US-09-904-859-64

US-09-904-86-64

US-09-904-786-64

US-09-904-786-64

US-09-904-786-64

US-09-907-796-64

US-09-907-794-64

US-09-907-794-64

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US-09-905-64
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Patent No. US20020076756A1
GENERAL INFORMATION:
   US-09-853-161-76
   Sequence 76, Appl
Sequence 30, Appl
Sequence 20, Appl
Sequence 2, Appli
Sequence 64, Appl
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Sequence 76, Appl
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2014.238 Million cell updates/sec
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                                                                                                                  December 9, 2003, 17:25:18 ; Search time 25.4843 Seconds
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276
1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-799-777-30
US-09-799-777-30
US-09-799-777-30
US-09-909-320-64
US-09-909-320-64
US-09-953-499-9
US-09-953-499-9
US-09-907-881-64
US-09-907-881-64
US-09-907-881-64
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                                                                                                                                                                                                                                                                                                   684280 seqs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                  OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match 1
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7:
111:
112:
113:
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115:
116:
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Score

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2230 2330 2330 2330 2330

Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

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TYPE: PRT
ORGANISM: Homo sapiens
                                                FEATURE:
NAME/KEY: SITE
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                 FEATURE:

NAME/KEY: SITE

LOCATION: (42)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (58)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Aaa equals any of the naturally occurring L-amino acids

US-09-853-161-76
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                                                                                                                                                                                                                                   Length 298
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100.0%; Pred. No. 4.5e-260;
iive 0; Mismatches 0;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILLING DATE: 2001-05-13
PRIOR PEDLICATION NUMBER: 60/265,583
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR PELLING DATE: 1988-09-11
PRIOR FILLING DATE: 1988-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR PELLING DATE: 1989-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR PELLING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR PELLING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-05
PRIOR PELLING DATE: 1997-05-05
PRIOR FILLING DATE: 1997-06-05
PRIOR FILLING DATE: 1997-05-05
PRIOR FILLING DATE: 1997-05-05
PRIOR PELLING DATE: 1997-01-09-05
PRIOR PELLING DATE: 1997-10-19
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Patent No. US20020077287A1
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Best Local Similarity 100.
Matches 276; Conservative
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 76
ORGANISM: Homo sapiens
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; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659A-76
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Best Local Similarity 100.0%; Pred. No. 4.5e-260;
Matches 276; Conservative 0; Mismatches 0;
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Patent No. US20020172994A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P2
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PRIOR APPLICATION NUMBER: US/09/852,797
CURRENT PILING DATE: 2001-05-11
PRIOR PLILING DATE: 2001-05-02
PRIOR PLILING DATE: 2001-02-02
PRIOR PLILING DATE: 1988-03-11
PRIOR PAPLICATION NUMBER: 09/152,060
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-05
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
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Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESSE:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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                                                                                                                                                                                                                                                                                 Query Match 87.0%; Score 240; DB 9; Length 298; Best Local Similarity 100.0%; Pred. No. 9.2e-227; Matches 240; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PErfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION: «Unknown»
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/002,485
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-745-763-38
                                               7) 498-8284
876-5851
                      TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 498-828
TELEFAX: (617) 876-5851
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Patent No. US20020001244A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
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Corley, Neil C.
Guegler, Karl J.
                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                        LENGTH: 298 amino acids
      REGISTRATION NUMBER:
                                                                                INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                DOCATION: (42)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (58)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-797-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFN 180
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                                                                                                                                                                                                                                                                                 Length 298;
                                                                                                                                                                                                                                                                           99.3%; Score 274; DB 10; Length 2 100.0%; Pred. No. 4.5e-260; ive 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 RKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
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APPLICATION NUMBER: US/09/745,763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sprunger, Suzanne A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merberg, David
Treacy, Maurice
Spaulding, Vikki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evans, Cheryl
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 276; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 02140
SOFTWARE: Patentin Ver.
SEQ ID NO 76
LENGTH: 298
                                                                          ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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US-09-745-763-38
                                                          TYPE: PRT
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Sequence 2, Application US/10192791
Sequence 2, Application US/10192791
Sequence 2, Application No. US20030130166A1
GENERAL INFORMATION:
APPLICANT: Texas Biotechnology Corporation
TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (J
TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (J
CURRENT PAPLICATION NUMBER: US/10/192,791
CURRENT FILING DATE: 2003-12-10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 298
                                                                                                                                                                                                                                                              59 SRLEWKKLGRSVSFVYYQQTLQGDFKARAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                                                                                                                                                                                                                                         QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156
                                                                                                                                                                                                                                                                                                                                               119 QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 178
                                                                                                                                                                                                                                                                                                                                                                                                         157 PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                     179 PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII 276
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o
                                                                                                                                                      Length 298;
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                                                                                                                                                                                           0; Indels
                                                                                                                                                 87.0%; Score 240; DB 15; L
100.0%; Pred. No. 9.2e-227;
Artive 0; Mismatches 0;
                                         TOPOLOGY: linear
MOLECULE TYPE: protein.
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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; Patent No. US20020132240A1
; GENERAL INFORMATION:
    acids
    LENGTH: 298 amino TYPE: amino acid
                                                                                                                                                                                           Matches 240; Conservative
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Matches 240; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                 Query Match
Best Local Similarity
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US-10-139-849-2
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                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                               Length 298;
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TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN
JUNCTIONAL ADHESION PROTEIN (JAM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
Suite 4700
                                                                                                                                                                                                                                                                                            Query Match
87.0%; Score 240; DB 9; Length 29
Best Local Similarity 100.0%; Pred. No. 9.2e-227;
Matches 240; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/139,849
FILING DATE: 07-May-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                     LIBRARY: DUODNOTO2
CLONE: 1704050
SEQUENCE DESCRIPTION: SEQ ID NO: 30 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/643,929
FILING DATE: 23-Aug-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                   TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                 LENGTH: 298 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10139849
Publication No. US20030079238A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                           STRANDEDNESS: single
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                                                                                                                                             TOPOLOGY: linear IMMEDIATE SOURCE:
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
                                                                                                                                                                                                                                                     US-09-799-777-30
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US-10-139-849-2
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SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
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                                                                                                                                                                                                                                                                        179 PRIGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNIS 238
                                                                                                                   QNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN 156
                                                                                                                                                                                                                                      PRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGBYSCEARNSVGYRRCPGKRMQVDDLNIS 216
SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                                                                                                                                         GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 266
                                                                                                                                                                                                                                                                                                                                                                                        239 GIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSEN 288
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CURRENT APPLICATION NUMBER: US/09/909,008BB
CURRENT FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US 60/414

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-13

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 64, Application US/0990908BB
Patent No. US20020146709A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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Hillan, Kenneth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Genentech, Inc.
APPLICANT: Ashkenzi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
APPLICANT: Baton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT APPLICATION NUMBER: US/09/414
FRIOR APPLICATION NUMBER: US 60/143,048
FRIOR FILING DATE: 2000-0-02-22
FRIOR PELING DATE: 1999-07-07
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR FILING DATE: 1999-07-07
FRIOR PELING DATE: 1999-07-07
FRIOR PELING DATE: 1999-07-08
FRIOR FILING DATE: 1999-07-08
FRIOR FILING DATE: 1999-09-13
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-11-20
FRIOR APPLICATION NUMBER: PCT/US99/28313
FRIOR FILING DATE: 1999-11-20
FRIOR APPLICATION NUMBER: PCT/US99/2865
FRIOR FILING DATE: 1999-11-20
FRIOR APPLICATION NUMBER: PCT/US99/28055
FRIOR APPLICATION NUMBER: PCT/US99/28055
FRIOR FILING DATE: 1999-11-20
FRIOR APPLICATION NUMBER: PCT/US99/28055
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-30
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 312
                                                                                                                                                                                                                                                                                 Godowski, Paul J.
Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                          Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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                        Desnoyers, Luc
Eaton, Dan L.
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COCGANISM: Homo sapiens
US-09-909-320-64
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                                              APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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59 SRLEWKKLGRSVSFVYYQQTLQGDFXNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 QNLEEDIVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG
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                  FILE REPERBUCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905, 291A

CURRENT APPLICATION NUMBER: US/09/905, 291A

CURRENT APPLICATION NUMBER: US/09/905, 291A

CURRENT APPLICATION NUMBER: DCT/USO0/04414

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-13

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PRIOR PLING DATE: 1999-09-15

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PRIOR PLING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR PRILOR PRIOR NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-20

PRIOR PRILOR DATE: 1999-11-20

PRIOR PRILOR DATE: 1999-11-30

PRIOR PRILOR DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-09

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PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-10-09

PRIOR FILING DATE: 1999-10-09

PRIOR PRIOR FILING DAT
TITLE OF INVENTION: Acids Encoding the Same
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 230; Conservative
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CORGANISM: Homo sapiens
US-09-905-291A-64
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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         FRIOR AFFLILATION WUNDER: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
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Patent No. US20020160374A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara, Napoleone
Filvaroff, Ellen
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Beton, Luc
APPLICANT: Baton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: FOUL, NATIONARY FOUR APPLICANT: FOUR APPLICANT: FOUR APPLICANT: Steart, Timothy A. APPLICANT: Steart, Timothy A. APPLICANT: Steart, Timothy A. APPLICANT: Steart, Timothy A. APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
ITILE DF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REBERNER: 10466-14
CURRENT APPLICANTON: ADMER: US/09/902,853
CURRENT APPLICANTON NUMBER: US/09/66,350
PRIOR PLING DATE: 2000-09-18 06/145,698
PRIOR PLING DATE: 108-00-18 06/145,698
PRIOR PLING DATE: 109-00-05
PRIOR PELICANTON NUMBER: US/09/902-09-09
PRIOR PELICANTON NUMBER: PCT/US99/2034
PRIOR PLING DATE: 1999-09-03
PRIOR PLING DATE: 1999-09-03
PRIOR PLING DATE: 1999-09-11-20
PRIOR PLING DATE: 1999-09-12
PRIOR PLING DATE: 1999-09-12
PRIOR PLING DATE: 1999-09-12
PRIOR PLING DATE: 1999-109-12
PRIOR PRIOR PELICANTON NUMBER: PCT/US99/2099
PRIOR PELICANTON NUMBER: PCT/US99/20999
PRIOR PELICANTON NUMBER: PCT/US99/20999
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Paoni, Nicholas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo Sapien
US-09-902-853-64
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TYPE: PRT
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Best Local S
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                                    APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Tunas, Daniel
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFERENCE: P121GR1(US)
CURRENT APPLICATION NUMBER: US/09/254,465
FRIOR APPLICATION NUMBER: D2001-09-14
FRIOR APPLICATION NUMBER: D2001-09-14
FRIOR PFLING DATE: 1998-11-07
FRIOR FILING DATE: 1998-11-07
FRIOR FILING DATE: 1998-11-07
FRIOR FILING DATE: 1998-13-07
FRIOR APPLICATION NUMBER: US 60/078,936
FRIOR APPLICATION NUMBER: PCT/US98/19437
FRIOR APPLICATION NUMBER: PCT/US98/19437
FRIOR APPLICATION NUMBER: PCT/US98/19437
FRIOR APPLICATION NUMBER: PCT/US98/19437
FRIOR FILING DATE: 1998-03-17
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Mather, Jennie P.
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ORGANISM: Homo sapiens
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US-09-902-853-64
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAFSEQG 118
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                        Length 312;
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                                                                                                                                     83.3%; Score 230; DB 10; I
100.0%; Pred. No. 6.1e-217;
iive 0; Mismatches 0;
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PRIOR FILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
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CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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Grimaldi, Christopher J.
Gurney, Auerin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Publication No. US20020198366A1
GENERAL INFORMATION:
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Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-64
                                                                                                                                   Query Match
Best Local Similarity
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PPLICANT: Wood, William, I.
IILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IILE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-02-18

PRIOR PELICATION NUMBER: PCT/US00/04114

PRIOR PELICATION NUMBER: PCT/US00/04114

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-09-18

PRIOR PELING DATE: 1999-09-19

PRIOR PELING DATE: 1999-09-19

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELICATION NUMBER: PCT/US99/21309

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-11-30

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-03

PRIOR PELING DATE: 1999-12-03
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CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
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PRIOR FILING DATE: 1999-12-20
PRIOR PELICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Grimaldi, Christopher J.
                                        Sequence 64, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
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Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Pan, James
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APPLICANT: Abhkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
PRIOR APPLICATION NUMBER: 09/665,350
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
REMAING APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
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Publication No. US20030003530A1
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferzara, Napoleone
APPLICANT: Filvaroff, Ellen
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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Mather, Jennie P.
                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-09-907-841-64
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59 SRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 118
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Best Local Similarity 100.0%; Pred. No. 6.1e-217;
Matches 230; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PLILING DATE: 2000-02-22
PRIOR PLILING DATE: 1990-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
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PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/20556
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-06
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Job time : 26.4843 secs
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ORGANISM: Homo Sapien
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GenCore version 5.1.6
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Run on:

OM protein - protein search, using sw model

December 9, 2003, 17:21:03 ; Search time 13.4634 Seconds (without alignments) 1971.458 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-852-797-76_COPY_23_298
276
1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276

OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

20

Word size :

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

4

0

Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description sult Query No. Score Match Length DB

Result

No matches found

Search completed: December 9, 2003, 17:25:56 Job time : 13.4634 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

9, 2003, 17:14:27; Search time 9.61672 Seconds (without alignments) 1349.666 Million cell updates/sec December

US-09-852-797-76_COPY_23_298 276 1 YHKAYGFSAPKDQQVVTAVX......SSKATTMSENDFKHTKSFII 276

Perfect score: Title:

Sequence:

Gapop 60.0 , Gapext 60.0 OLIGO Scoring table:

127863 seqs, 47026705 residues

20 Word size :

Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		P57087 homo sapie
ID		240 87.0 298 1 JAM2_HUMAN
DB	1	-
Length		298
Match	1 1 1 1 1 1	87.0
Score		240
No.	1 1 1 1	1
	No. Score Match Length DB ID Description	No. Score Match Length DB ID Description

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ALIGNMENTS

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TISSUE-Vascular endothelial cells;
MEDLINE=20317114; PubMed=10779521;
Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
"Vascular endothelial junction-associated molecule, a novel member the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells.";
J. Biol. Chem. 275:19139-19145(2000).
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                            Ź
                       298
                       PRT;
                                                                                                                                                                                                                                                                           TISSUE=Placenta;
MEDLINE=20507930; PubMed=10945976;
                       STANDARD;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                            NCBI_TaxID=9606;
                      HUMAN
                    JAM2 HL
P57087;
            JAM2_HUMAN
RESULT 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjercke R.J., Vanderslice P., Morris A.P., Brock T.A.; "A novel protein with homology to the junctional adhesion molecule: Characterization of leukocyte interactions."; J. Biol. Chem. 275:34750-34756 (2000).
                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUB SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
--- TISSUB SPECIFICITY: PROMINENTLY EXPORTHELIA OF OTHER VESSELS.
LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE IMMUNOSLOBULIN SULENTED.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- DATABASE: NAME=PROW; NOTE=PROW 2:1-3 (2001);
WWW-nhttp://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 606370; -...
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0015837; P:cell-cell adhesion; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003589; Ig-2.
InterPro; IPR003006; Ig-MHC.
Ffam; PF00047; Ig; 2.
FRWST; SM00408; IG-2: 1.
PROSITE; PS50835; IG-LIKE; 2.
Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUNCTIONAL ADHESION MOLECULE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY016009; AAG49022.1; -. EMBL; BC017779; AAH17779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:14686; JAM2.
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238
2298
2298
2238
2109
                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                           0; Gaps
98 98 N-LINKED (GLCNAC. ..) (POTENTIAL)
187 187 N-LINKED (GLCNAC. ..) (POTENTIAL)
236 236 N-LINKED (GLCNAC. ..) (POTENTIAL)
298 AA, 33207 MW, CA78E518E22DCAEE CRC64;
                                                  Query Match 87.0%; Score 240; DB 1; Length 298; Best Local Similarity 100.0%; Pred. No. 1.6e-232; Matches 240; Conservative 0; Mismatches 0; Indels
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Search completed: December 9, 2003, 17:24:01 Job time : 9.61672 secs

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December 9, 2003, 17:20:17; Search time 29.8118 Seconds (without alignments) 2389.068 Million cell updates/sec
                                                                                                                                                                                                                                                                           276
1 YHKAYGFSAPKDQQVVTAVX.....SSKATTMSENDFKHTKSFII 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                            830525 seqs, 258052604 residues
                                                                                                                                                                                                                                             US-09-852-797-76_COPY_23_298
                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: sp_archea:*
2: sp_bacteria:*
3: sp_lungi:*
4: sp_lummn:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mnamal:*
7: sp_mnamal:*
7: sp_mnamal:*
7: sp_nto:*
8: sp_organelle:*
9: sp_plant:*
1: sp_organelle:*
1: sp_organelle:*
1: sp_organelle:*
1: sp_organelle:*
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2: sp_ortebrate:*
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3: sp_ortebrate:*
5: sp_ortebrate:*
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Word size
                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ouery Score Match Length DB ID

Description

No smatches found

Result No. Search completed: December 9, 2003, 17:25:15 Job time : 29.8118 secs